



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 182281

TO: Phuong Bui
Location: REM/2A15/2C18
Art Unit: 1638
Friday, March 17, 2006
Case Serial Number: 09/938294

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518

BOB
barbara.obryen@uspto.gov

Search Notes

RUSH

This Page Blank (uspto)

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 16, 2006, 23:57:28 ; Search time 8728 Seconds
(without alignments)
11084.734 Million cell updates/sec

Title: US-09-938-294-2

Perfect score: 1702

Sequence: 1 attcgcgtgagttgatcc.....gaggagattcaatttagt 1702

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 588141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_in.*
- 3: gb_env.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sta.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vi.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1019.4	59.9	1120	BT017155	BT017155 Zea mays
2	664	39.0	2069	BT013466	BT013466 Lycopersi
3	602.4	35.4	1695	AK176263	AK176263 Arabidops
4	602.4	35.4	1709	AK176210	AK176210 Arabidops
5	590.8	34.7	1765	BT008621	BT008621 Arabidops
6	282.6	16.6	90341	AC024609	AC024609 Arabidops
7	282.6	16.6	119942	AC007797	AC007797 Arabidops
8	253.4	14.9	100685	AC023754	AC023754 Arabidops
9	224.8	13.2	110000	AP008207	Continuation (89 o
10	224.8	13.2	146081	AP001366	AP001366 Oryza sat
11	158.6	9.3	92376	AP008071	AP008071 Lotus cor
12	115.2	6.8	92376	AP008071	AP008071 Lotus cor
13	93	5.5	2013	BT008418	BT008418 Arabidops
14	93	5.5	2603	BT002514	BT002514 Arabidops
15	90.2	5.3	1172	AK221889	AK221889 Arabidops
16	89.4	5.3	2124	ATH507211	ATH507211 Arabidops
17	89.4	5.3	2557	AY091763	AY091763 Arabidops
18	87.8	5.2	75948	AC037424	AC037424 Arabidops

c 19	87.8	5.2	117737	15	F6D8	AC008016 Arabidops
c 20	65.8	3.9	147292	14	AC023010	AC023010 Homo sapi
c 21	60	3.5	5445	15	AK121451	AK121451 Oryza sat
c 22	60	3.5	110000	15	AP008209	Continuation (24 o
c 23	60	3.5	150503	15	AC122149	AC122149 Oryza sat
c 24	58.2	3.4	42273	15	NCB12N19	AL669987 Neurospor
c 25	58.2	3.4	122151	15	NCB23H20	AL669988 Neurospor
c 26	56.4	3.3	35762	15	AB026653	AB026653 Arabidops
c 27	56	3.3	1478	15	AK099685	AK099685 Oryza sat
c 28	56	3.3	70311	15	AF128457	AF128457 Oryza sat
c 29	56	3.3	77605	15	AF119222	AF119222 Oryza sat
c 30	56	3.3	110000	15	AP008217	Continuation (234
c 31	56	3.3	142852	15	AF161269	AF161269 Oryza sat
c 32	55.6	3.3	48144	14	AC069166	AC069166 Homo sapi
c 33	54.4	3.2	1555	15	AK106377	AK106377 Oryza sat
c 34	54	3.2	85813	15	AP006644	AP006644 Lotus cor
c 35	53.6	3.1	129886	14	AC148571	AC148571 Taeniopyg
c 36	53.2	3.1	110000	15	AE017348	Continuation (10 o
c 37	53.2	3.1	148061	14	CR848712	CR848712 Danio rer
c 38	53.2	3.1	110000	15	AP008217	Continuation (11 o
c 39	53	3.1	110000	15	AP008217	Continuation (18 o
c 40	53	3.1	149493	15	AC123528	AC123528 Oryza sat
c 41	53	3.1	305296	14	AC152796	AC152796 Bos tauru
c 42	53	3.1	321250	1	SC093911	AL52789 Bos tauru
c 43	53	3.1	345865	14	AC152789	AL684743 Penicilli
c 44	52	3.1	956	10	PM2D12B	AK120574 Oryza sat
c 45	52	3.1	2037	15	AK120574	

ALIGNMENTS

BT017155	1120 bp	mRNA	linear	PLN 27-OCT-2004
Zea mays clone EL01N0367F09.c	mRNA sequence.			
BT017155	BT017155.1 GI:54651936			
FLI CDNA.				
Zea mays				
ORGANISM				

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

Lai, J., Dey, N., Kim, C.-S., Bharti, A.K., Rudd, S., Mayer, K.F.X.,

Larkins, B., Bera, P. and Messing, J.

Characterization of the maize endosperm transcriptome and its comparison to the rice genome

Unpublished

2 (bases 1 to 1120)

Lai, J., Dey, N., Kim, C.-S., Bharti, A.K., Rudd, S., Mayer, K.F.X.,

Larkins, B., Bera, P. and Messing, J.

Direct Submission

Submitted (27-OCT-2004) Waksman Institute, Rutgers University, 190

Frelinghuysen Rd, Piscataway, NJ 08854, USA

Location/Qualifiers

1..1120

/organism="Zea mays"

/mol_type="mRNA"

/db_xref="taxon:4577"

/clone="EL01N0367F09.c"

ORIGIN

Query Match 59.9%; Score 1019.4; DB 15; Length 1120;

Best Local Similarity 97.7%; Pred. No. 2.1e-194;

Matches 1058; Conservative 0; Mismatches 16; Indels 9; Gaps 2;

575 GAAGATCATGTTCCTAAAGTCCTTCCGAAGATTTTGTGGTGCATCCATGAATCGTGG 634

9 GATGATCATGTTCCTAAAGTCCTTCCGAAGATTTTGTGGTGCATCCATGAATCGTGG 68

635 GCATTACTTTAAGTTGAATATGTCAACATCTCCCTTTGTTGCTGGAGCCATGATTGA 694

Db	69	GCATTACTTTAAGGTTGGAATATGTCAAACATCTTCCCTTTGTTGCTGGAGCCATGATTTGA	128
Qy	695	TTCTCATACAACGGCTGAGTATTGGAATAGCAGGACTAGCGATCGCTGAAAAATACAGAT	754
Db	129	TTCTCATACAACGGCTGAGTATTGGAATAGCAGGACTAGCGATCGCTGAAAAATACAGAT	188
Qy	755	GCCACAAACTTATGTTGTTCCACTGGGGAATAGTAAAGAACTAATGGAAGTGTGCTGAAGA	814
Db	189	GCCACAAACTTATGTTGTTCCACTGGGGAATAGTAAAGAACTAATGGAAGTGTGCTGAAGA	248
Qy	815	CAATGTCGGAAGAGTCTTACGGGAAACATATTCGTGGAATCCCTTGGAGTACGGAGTGA	874
Db	249	CAATGTCGGAAGAGTCTTACGGGAAACATATTCGTGGAATCCCTTGGAGTACGGAGTGA	308
Qy	875	GGATCTCTGTTTGCATATATAACAGTGTATCACGAGGAAGGGAACAAGACTTATTTTCT	934
Db	309	GGATCTCTGTTTGCATATATAACAGTGTATCACGAGGAAGGGAACAAGACTTATTTTCT	368
Qy	935	TCAAGCAATTTATCAGGCTTTTGCAGCTCATCCAAACACGAGAAACTTAAAGTGCGCTAGAAT	994
Db	369	TCAAGCAATTTATCAGGCTTTTGCAGCTCATCCAAACACGAGAAACTTAAAGTGCGCTAGAAT	428
Qy	995	ACATGCTGTAGTTGTGGGAAGTGAATTAATGCTCAGACCAAAATTTGAGACTCAGTTACG	1054
Db	429	ACATGCTGTAGTTGTGGGAAGTGAATTAATGCTCAGACCAAAATTTGAGACTCAGTTACG	488
Qy	1055	TGACTTTGCTGTGAAGAACAGATTCAATGACCGTGTCATTTTGTGAACAAGACATTTGGC	1114
Db	489	TGACTTTGCTGTGAAGAACAGATTCAATGACCGTGTCATTTTGTGAACAAGACATTTGGC	548
Qy	1115	AGTGGCCCCTTACTTGGCAGCAATTTGATGCTGTTGTTTCAAGAACTCTCAGGGCCGTGAGA	1174
Db	549	AGTGGCCCCTTACTTGGCAGCAATTTGATGCTGTTGTTTCAAGAACTCTCAGGGCCGTGAGA	608
Qy	1175	ATGCTTTTGAAGGATACAAATTGAAGCAA-TGGCAATTCAGTTGCCAGTATTGGGCACGG	1233
Db	609	ATGCTTTTGAAGGATACAAATTGAAGCAA-TGGCAATTCAGTTGCCAGTATTGGGCACGG	668
Qy	1234	CTGCTGAGGGACCAACGAGATCGTCTGGAACGGCTCGACTGGGCTTCTGTCATCCTGCTG	1293
Db	669	CTGCTGAGGGACCAACGAGATCGTCTGGAACGGCTCGACTGGGCTTCTGTCATCCTGCTG	728
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Db	729	GGAAGGAGGGCGTGGCCGCTCTTGCAAGAAACATCGTCAGACTCGCAAGCCACGCCGAGC	788
Qy	1354	AGAGGCTCCATGGGGGAAAGGGCTATGCGAGGGTGAAGGAATGTTCAATGGAGCACC	1413
Db	789	AGAGGCTCCATGGGGGAAAGGGCTATGCGAGGGTGAAGGAATGTTCAATGGAGCACC	848
Qy	1414	ACATGGCTGAGAGGATCCGCGCGTGTGAAGGATGTCTGAGGAAATTCACAGGAGCACT	1473
Db	849	ACATGGCTGAGAGGATCCGCGCGTGTGAAGGATGTCTGAGGAAATTCACAGGAGCACT	908
Qy	1474	CCAGGCTGTGAGCTTTGCGGTGCCCATCGCTTCGGCTAACATGTTGAACTTAGATTTTAC	1533
Db	909	CCAGGCTGTGAGCTTTGCGGTGCCCATCGCTTCGGCTAACATGTTGAACTTAGATTTTAC	968
Qy	1534	GGGCTACGCCCTACGTGGTTACGGCTGTAAACTGTAGATTGCACTCTGTGGTCTACTTTT	1593
Db	969	GAGCTACGCCCTACGTGGTTACGGCTGTAAACTGTAGATTGCACTCTGTGGTCTACTTTT	1028
Qy	1594	TCACATTTCA-----TGTTTTTACCTATTAGGCCATGTCCGATTTCTATTCCAAATTCATA	1645
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Qy	1646	TAG 1648	
Db	1089	TAG 1091	

BT013466	BT013466	2069 bp	mRNA	linear	PLN 11-MAY-2004
LOCUS	Lycopersicon esculentum clone J32125F, mRNA sequence.				
DEFINITION	Lycopersicon esculentum clone J32125F, mRNA sequence.				
ACCESSION	BT013466				
VERSION	BT013466.1	GI:47104881			
KEYWORDS	FLU_CDNA:				
SOURCE	Lycopersicon esculentum (Solanum lycopersicum)				
ORGANISM	Lycopersicon esculentum				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.				
REFERENCE	1. (bases 1 to 2069)				
AUTHORS	Kirkness, E.P., Wang, W. and Vazeille, A.				
TITLE	Direct Submission				
JOURNAL	Submitted (11-MAY-2004) The Institute for Genomic Research, 9712 Medical Center Drive, Rockville, MD 20850, USA				
FEATURES	Location/Qualifiers				
source	1..2069				
	/organism="Lycopersicon esculentum"				
	/mol_type="mRNA"				
	/db_xref="taxon:4081"				
	/clone="J32125F"				
	/tissue_type="fruit"				
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ORIGIN					
Query Match	39.0%;	Score 664;	DB 15;	Length 2069;	
Best Local Similarity	71.4%;	Pred. No. 6.1e-123;			
Matches	874;	Conservative 0;	Mismatches 350;	Indels 0;	Gaps 0;
Qy	266	GAGTCCCTCGGTT	CATGAGGTC	CAAGGTCGTC	TCCTGTCCTCCATGAGCTCTCCCT 325
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Qy	326	CTCTGGTGTCCATTTT	TACTGATGAA	TAGCAATTTCTTCTGAGGCATGTTGGCTCGCA 385	
Db	682	TTCTGGTGGACCTCT	GTGTGTGTGATGAGCT	TGGCAATTTTGTGAGAGGTTTTCGTGCTGA 741	
Qy	386	AGTGGTGTGATAA	CAAAACCAGAGAT	CACAAGAAACAAATGATGCACATATAGCTTGA 445	
Db	742	AGTCTGTTGATC	ACAAATCAAGGCCA	CTGAAACAAATACATTTGATACAGTTTGA 801	
Qy	446	GCATAGGATGTTGA	ACCATGAGCTG	CAGGTTTTTACCAGCTAGAGGACAGGAGCAGTTGA 505	
Db	802	GCACAAATGTTAC	CCGAGGAGTTC	CAGGTGTTCTCTCGAAGGGCCAGGAGCAATAGA 861	
Qy	506	TATTGCTCTAAA	AGCTGATCTGTTAT	TCTTAAACACTGTGTTGCTGGCAAGTGGCTTGA 565	
Db	862	TACTGCTTTGAAA	AGCTGACTTGGTTGT	TTTAAACACTGCGCGTTGCTGGGAAATGGTGTGA 921	
Qy	566	CCCTGTTCTCAA	AGATCATCTGTTCT	TAAGTCTTCGGAAGATTTTGTGGTGGATCCATGA 625	
Db	922	TGCTGTTCTTAA	AGAACACGTTTCT	GAGTCCCTTTCCTTGTGCTGGAGC 685	
Qy	626	AATGCGTGGCAT	TATCTTTAAGGT	TGAAATGTC	CAACATCTTCCCTTTGTGCTGGAGC 685
Db	982	AATGCGGGTCAT	TACTTCTAGTCT	TAGATTATG	TGAACACCTTCCATATGTTCTGTGTGC 1041
Qy	686	CATGATTGATTC	ATACAAACGGGT	GATGATTTGGAAT	TAGCAGACTAGCGATCGCTCGAA 745
Db	1042	AATGATTGATTCA	TGTAACAGTCT	GAATCTGGAAGAA	TAGGACACAGGAACGGCTAAG 1101
Qy	746	AATACAGATCC	CAACATTTATGTT	GTTCACCTGGGGA	TAGTAAAGAACTAATGGAAGT 805
Db	1102	GATCAAAATGCC	AAACCCCATGCT	GTTCATCTTTGG	CAACGCAATGAGCTATGGAAT 1161
Qy	806	TGCTGAAGACA	ATGTCGCAAGAG	GTCTTACGGGA	ACATATTCGTGAATCCCTTGGAGT 865
Db	1162	TGCTGAGATAG	TGTCGCAAA	AGGATTTT	TGAGGGAGCATGTTTCGTGAATCTCTTTGAGT 1221
Qy	866	ACGAGGTGAG	GATCTCCTGTTT	GCATAATA	TAAACAGTGTATACAGGAGAAAGGACAAGA 925
Db	1222	TCGAAACGAA	GATATATCTGTT	CTCCCTCAT	TAAATAGTGTACTCTGTGGGAAGGCTCAAGA 1281

URL:<http://range.gsc.riken.jp/>, Tel:81-45-503-9625,
Fax:81-45-503-9586)

FEATURES

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JRES      Location/Qualifiers
1..1695   /organism="Arabidopsis thaliana"
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1..1695   /gene="At1g19710"
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          /db_xref="GI:51970668"
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          WKNTHDRGLGIMKPTIVVHLGNSKELMEVGE
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ORIGIN

Query Match	35.4%	Score 602.4	DB 15	Length 1695
Best Local Similarity	69.1%	Pred. No. 1.5e-110		
Matches	838	Conservative 0	Mismatches 371	Indels 3
			Gaps 1	
Qy	266	GAGTCCCTCGGGTTTCATGAGTCCAAAGCTCGTGCCTCCTCCTCCATGAGCTCCTCCCT	325	
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Qy	326	CTCTGCTGTGCACACTTTTACTTGATGGAAATTAGCAATTTCTCTGAGGCATGTTGGCTCGCA	385	
Db	349	CTCAGGTGACCTTTATTTGTTAATGGAATGGCGTTTTTCTTAGAGGATTTGAATCTGA	408	
Qy	386	AGTGGTGTGGATAACAAACCAGAGATCACAGAAGAAATGATGTCCACATATAGCTTGA	445	
Db	409	AGTTGTTTGGATCACGAATCAGAAACCAAGTTGAAGAAGATGAAGTGATCAAGTTTCTAGA	468	
Qy	446	GCATAGGATTTGAACCATGAGTGCAGGTTTTTACAGCTAGAGGACAGAGGCAGCTTGA	505	
Db	469	ACACAAGATGTTGGATCGAGGAGTCCAGGTGATATCAGCAAAAGAGTCAAGAAAGCTATAGA	528	
Qy	506	TATTGCTCTAAAAGCTGATCTGGTTATCTTAAACACTGCTGTGCTGGCAAGTGGCTTGA	565	
Db	529	TACAGCTCTCAAGTCTGATCTGGTTGTTTTTAAACACTGCTGTGCTGGGAAATGGCTTGA	588	
Qy	566	CCCTGTTCTTGAAGATCATGTTCTCTAAAGTCCTTCGGAAGATTTTCTGGTGGATCCATGA	625	
Db	589	TGCAGTTCTCAAGGACAAATGTTCTTAAGTTCCTTAAAGTACTCTGGTGGATTCATGA	648	
Qy	626	AATGCGTGGGCATTACTTTAAGTTGGAATATGTCAAACATCTTCCCTTTTGTGCTGGAGC	685	
Db	649	GATGAGAGGTCACTATTTCAAACCGGATTTAGTCAAGCACCTTCCTCGTTGTTGCGAGTGC	708	
Qy	686	CATGATTGATTTCTCATACAACCGCTGAGTATTGGAAATAGCAGGACTAGCGATCGCCTGAA	745	
Db	709	TATGATTGATTGCGACGCAACAGCTGAATACATCTGGAAAGAACAGAACTCATGATCGCTTAGG	768	

926	Qy	CTTATTTCTTCAAGCATTTTATCAGGCTTTGACGCTCATCAACACAGAGAAACTTAAAGT	985
1282	Db	 CTTATTTTATCGGTCGTTTTATGAGAGCTTGCAGATTAITCAAGAAACGGAGTTACAAAT	1341
986	Qy	GCCTAGAAATACATGCTCTAGTTGTTGGGAAGTGATGTTAATGCTCAGACACAAATTTTGAGAC	1045
1342	Db	 ACCATCAATTCATGCTGTTGTTGAGGAGTGACATGACTAGTCATAGTAAATTTTGAGAC	1401
1046	Qy	TCAGTTACGTCACTTTCTGGTGAAGAACACGATTCATGACCGTGTCOAATTTGTGAACAA	1105
1402	Db	AGAGCTTAGGAACTTTTGTCATATCAAAAGAAGATCCAGAAATATGTTCAATTTGTTAATAA	1461
1106	Qy	GACATTTGGCAGTGGCCCCCTTACTTTGGCAGCAATTGATGCTGTTGTCAGAAATTTCTCAGGG	1165
1462	Db	GACACTCACGGTAGCCCCATCTTTGCTGCAGTTGATGTTCTTTGTTTCAGAAATTTCTCAGGC	1521
1166	Qy	CCGTGGAGAAATGCTTTTGGAAGGATAACAAATTTGAAGCAATGGCATTCCAAGTTGCCAGTATT	1225
1522	Db	ACGAGTGAAATGCTTTTGTTAGATTACTATTTGAGCGATGGCGTTTCAGCTGCTGTGTT	1581
1226	Qy	GGGCACGGCTGCTGGAGGAGCACCGAGATCGTCTCTGGACGGTTCGACTGGCCCTTCTGCA	1285
1582	Db	GGGAACCTGCTGCTGGTGGCACCACAGAAATGTAAACAAATGGAACAACTGGTCTTCTACA	1641
1286	Qy	TCCTGCTGGGAAGGAGGGCGTGCGCCTCTTTGCAAAGAAACATCGTCAGACTCGCAAGCCA	1345
1642	Db	TCCTGTGGGGAAGAAGGGATAATGCCCTCTTGCAAAAAACATTTAGATTAGCCACTCA	1701
1346	Qy	CGCCGACGAGGGTCTCCATGGGGGAAAAGGGCTATGGCAGGGTGAGGAAATGTTTCAT	1405
1702	Db	CGTTGAGGAGGGCTTCAATATGGGTAAAAAGGGTATGGAAGGTTTAAAGAGACTTTTCT	1761
1406	Qy	GGAGCACCAATATGGCTCAGAGGATCGCGGGGTGTTTCAAGGATGTCCTGAGGAAATCACA	1465
1762	Db	GGAGCATCATATGGAAGAAAGAAATTCAGGAGTTCTAAAGGACGTGTTGCAGAAAGCAAT	1821
1466	Qy	GGAGCACTCCAGGTCCTTGAGCTTT	1489
1822	Db	GGAACTCAAAGGACATGATAAT	1845

RESULT 3	
AKI76263	
LOCUS	1695 bp mRNA linear PLN 09-SEP-2004
DEFINITION	Arabidopsis thaliana mRNA for hypothetical protein, complete cds, clone: RAFL23-16-P14.
ACCESSION	AKI76263
VERSION	AKI76263.1 GI:51970667
KEYWORDS	FLU CDNA.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE	1
AUTHORS	Totoki, Y., Seki, M., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Shin-i, T., Nakagawa, M., Sakamoto, N., Oishi, K., Kohara, Y., Kobayashi, M., Toyoda, A., Sakaki, Y., Sakurai, T., Iida, K., Akiyama, K., Satou, M., Toyoda, T., Konagaya, A., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
TITLE	Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1695)
AUTHORS	Totoki, Y., Seki, M., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Shin-i, T., Nakagawa, M., Sakamoto, N., Oishi, K., Kohara, Y., Kobayashi, M., Toyoda, A., Sakaki, Y., Sakurai, T., Iida, K., Akiyama, K., Satou, M., Toyoda, T., Konagaya, A., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
TITLE	Direct Submission
JOURNAL	Submitted (06-SEP-2004) Motoaki Seki, RIKEN Genomic Sciences Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:mseki@gsc.riken.jp).

QY	746	AATACAGATGCCAAACTTATGTTGTTTCACTGGGGAATAGTAAGAACTAATGAAGT	805	TITLE	Large-scale analysis of RIKEN Arabidopsis full-length (RAPL) cDNAs
Db	769	GATTAATAGCCCTAAACTTATGTTGTTGACCTAGCACTAGCAAGAGTGTGAGT	828	JOURNAL	Unpublished
QY	806	TGCTGAAGCAATGTCCGAAGAGTCTCTACGGGAACATATTCGTGAATCCCTGGAGT	865	REFERENCE	2 (bases 1 to 1709)
Db	829	AGCTGAAGATAGTTTCCGCAAGATGTTCTCCGTGAGCAAGTTCGAGAACTCTCTGGAGT	888	AUTHORS	Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A., Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y., Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K., Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J., Hayashizaki Y. and Shinozaki K.
QY	866	ACGGAGTGAAGTCTCTCTTTCATATAACAGATGTATCACAGGGAAGGCAAGA	925		Direct Submission
Db	889	GAGGAATGAAGACATATCTATTTGGCAATTAATAGTGTATCTCGAGGAAGGCGCAAGA	948		Submitted (06-SEP-2004) Motoaki Seki, RIKEN Genomic Sciences Center, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:msk1gsc.riken.jp, URL:http://range.gsc.riken.jp/, Tel:81-45-503-9625, Fax:81-45-503-9586)
QY	926	CTTATTTCTTCAAGCATTTTATCAGGCTTTCAGACTCATCCAACTA	982	COMMENT	An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI and XhoI was ligated to modified lambda PhiC-E vector (Carninci et al. (2001) Genomics 77:79-90) digested with BamHI and SalI. This clone is in a modified pBluescript vector.
Db	949	TCTATTTCTCCGAGCGTTCCTGAAAGTCTTAAGTAATCAAGAGACTAAGAACTTGA	1008		Please visit our web site (http://range.gsc.riken.jp/) for further details.
QY	983	AGTGCTAGAAATACATGCTGTAGTGTGGGAAGTGAATTAATGCTCAGACCAAAATTTGA	1042	FEATURES	Location/Qualifiers
Db	1009	GGTACCACAAATGATGCTAGTGTAGTGAAGCGATATGAGCGCACAGCAAAATTTGA	1068	source	1..1709
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AUTHORS					

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Arabidopsis thaliana chromosome I BAC F14P1 genomic sequence, complete sequence.				
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AC024609.2	GI:7212002			
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Arabidopsis thaliana (thale cress)				
Arabidopsis thaliana				
Accession				
Version				
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Organism				
Reference				
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Journal				
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1 (bases 1 to 90341)
 Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
 Altafi, H., Nguyen, M., Lam, B., Southwick, A., Miranda, M., Brooks, S.,
 Buehler, E., Chao, Q., Chin, C., Chou, J., Choi, E., Gonzalez, A.,
 Hwang, B., Johnson-Hopson, C., Khan, S., Kim, C., Koo, T., Lee, J.M.,
 Lenz, C., Liu, A., Liu, S., Mukharshy, N., Pham, P., Sakano, H.,
 Shinn, P., Toriumi, M., Vaysberg, M., Walker, M., Yu, G., Ecker, J.,
 Theologis, A., and Davis, R.W.
 Unpublished
 2 (bases 1 to 90341)
 Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
 Altafi, H., Nguyen, M., Lam, B., Southwick, A., Bei, Q., Buehler, E.,
 Chin, C., Chou, J., Choi, E., Dunn, P., Gonzalez, A., Hwang, B., Kim, C.,
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 Theologis, A., Toriumi, M., Vaysberg, M., Walker, M., Yu, G., Ecker, J.,
 Theologis, A., and Davis, R.W.
 Direct Submission
 Submitted (01-MAR-2000) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 3 (bases 1 to 90341)
 Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
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 Direct Submission
 Submitted (09-MAR-2000) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 4 (bases 1 to 90341)
 Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,

Altafi, H., Nguyen, M., Lam, B., Southwick, A., Ecker, J., Theologis, A. and Davis, R.W.

TITLE JOURNAL

Submitted (11-AUG-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA

5 (bases 1 to 90341)

REFERENCE AUTHORS

Pederspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
Altafi, H., Nguyen, M., Lam, B., Southwick, A., Ecker, J., Theologis, A.
and Davis, R.W.

TITLE JOURNAL

Submitted (12-SEP-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA

COMMENT

On Mar 9, 2000 this sequence version replaced gi:7121532.
Bases 1-59,676 of IGF clone F14P1 overlap with IGF clone F6F9,
gb|AC007797.

e-mail for correspondence: arab@sequence.stanford.edu
Genes with similarity to proteins in the databases are named
'putative', '-like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'. The
gene prediction programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
<http://combio.ornl.gov/section/index.html>), GENSCAN (Chris Burge,
<http://genome.stanford.edu/~chris/GENSCANW.html>), and NetPlantGene
(S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, <http://www.cbs.dtu.dk/NetPlantGene.html>).

FEATURES

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ISAIETVATDATGAGDLFGLYGLIKLSLEECCKVSGSGSGVTEVTPTE

TITLE Direct Submission
JOURNAL Submitted (12-SEP-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA

COMMENT On May 16, 2000 this sequence version replaced gi:7547094.
Bases 60,267-119,942 of BAC clone F6F9 overlap with bases 1-59,676
of IGF clone F14P1, AC024609 and bases 1-3,490 of BAC clone F6F9
overlap with bases 81,221-92,710 of BAC clone T20H2, AC022472.

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Best Local Similarity	65.48;	Pred. No. 2.6e-40;		
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901	GTGTATCAGCAGGAAAGGACAAAGACTTATTTCTTCAAGCATTTTATCAGGCTTTTCGACG	960		
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WPCOMMENT
Sequence split into 433 fragments LOCUS AP008207 Accession AP008207

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RESULT 10

AP001366/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1

Sasaki, T., Matsumoto, T., Yamamoto, K., Sakata, K., Baba, T.,

Katayose, Y., Wu, J., Niimura, Y., Cheng, Z., Nagamura, Y.,

Antonio, B. A., Kanamori, H., Hosokawa, S., Masukawa, M., Arikawa, K.,

Chiden, Y., Hayashi, M., Okamoto, M., Ando, T., Aoki, H., Arita, K.,

Hamada, M., Harada, C., Hijishita, S., Honda, M., Ichikawa, Y.,

Idonuma, A., Iijima, M., Ikeda, M., Ikono, M., Ito, S., Ito, Y.,

Ito, Y., Iwabuchi, A., Kamiya, K., Karasawa, W., Katagiri, S.,

Kikuta, A., Kobayashi, N., Kono, I., Machita, K., Maehara, T.,

Mizuno, H., Mizubayashi, T., Mukai, Y., Nagasaki, H., Nakashima, M.,

Nakano, H., Nakamichi, Y., Nakamura, M., Namiki, N., Negishi, M.,

Ohta, I., Ono, N., Saji, S., Sakai, K., Shibata, K., Shimokawa, T.,

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Yamagata, H., Yamane, H., Yoshiki, S., Yoshihara, R., Yukawa, K.,

Zhong, H., Iwama, H., Endo, T., Ito, H., Hahn, J. H., Kim, H. I., Eun, M. Y.,

Yano, M., Jiang, J. and Gojobori, T.

The genome sequence and structure of rice chromosome 1

Nature 420 (6913), 312-316 (2002)

12447438

2 (bases 1 to 146081)

Sasaki, T., Matsumoto, T. and Yamamoto, K.

Direct Submission

Submitted (09-MAR-2000) Takuji Sasaki, National Institute of

Agrobiological Sciences, Rice Genome Research Program; Kannondai

2-1-2, Tsukuba, Ibaraki, 305-8602, Japan

(E-mail: tsasaaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/,

Tel: 81-298-38-7441, Fax: 81-298-38-7468)

Genes were predicted from the integrated results of the following:

GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH

(http://www.softberry.com/), GeneMark.hmm

(http://opal.biology.gatech.edu/GeneMark/), GlimmerM

(http://www.tigr.org/cdb/glimmer/glmr_form.html), RiceHMM

(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor

(http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4

(http://globin.cse.psu.edu/html/docs/sim4.html), gap2

(http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The

genomic sequence was searched against NCBI NonRedundant Protein

database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA

sequence database at RGP or DDBJ. Protein homologues of the coding

regions were searched against NCBI NonRedundant Protein database

with BLASTP. ESTs represent the identified cDNA sequences using

BLASTN with the corresponding DDBJ accession no. and RGP clone ID.

Full-length cDNAs represent the identified cDNA sequences using

BLASTN with the corresponding DDBJ accession no.

A gene with identity or significant homology to a protein is

classified based on the protein name to indicate the homology level

such as same name, 'putative-' and '-like protein'. A gene without

significant homology to any protein but with full-length cDNA or

EST homology (covering almost the entire length of partial

sequence) is classified as an 'unknown' protein. A gene predicted

by two or more gene prediction programs is classified as a

'hypothetical' protein according to IRGSP standard. A gene

predicted by a single gene prediction program is also classified as

a probable 'hypothetical' protein and is included as a

miscellaneous feature of the sequence.

The orientation of the sequence is from SP6 to T7 of the PAC clone.

This sequence of P0469E09 clone has an overlap with P0699D11 (DDBJ:

AP002817) clone at 5' end and with P0453A06 (DDBJ: AP001383) clone

at 3' end. Detailed information on overlap and assembly quality

together with annotation of this entry is available at

http://rgp.dna.affrc.go.jp/GenomeSeq.html.

FEATURES

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 VERSION AP008071.1 GI:56806379
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 SOURCE Lotus corniculatus var. japonicus (Lotus japonicus)
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
 Lotus.
 REFERENCE 1
 AUTHORS Kaneko, T., Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
 TITLE Structural Analysis of a Lotus japonicus Genome. XI. Sequence
 Features and Mapping of Nine hundred twenty-one TAC Clones
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 92376)
 AUTHORS Sato, S.
 TITLE Direct Submission
 JOURNAL Submitted (26-OCT-2004) Shusei Sato, Kazusa DNA Research Institute,
 Department of Plant Gene Research, 2-6-7 Kazusa-kamatari, Kisarazu,
 Chiba, 292-0818, Japan [E-mail: ssato@kazusa.or.jp,
 URL: http://www.kazusa.or.jp/, Tel: 81-438-52-3935 (ex. 2337),
 Fax: 81-438-52-3934)
 COMMENT
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 21 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
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 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
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RESULT 13

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ACCESSION BT008418
VERSION 1
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SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 2013)
AUTHORS Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Carninci,P.,
Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T.,
Kamaya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lin,J., Miranda,M.,
Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L.,
Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Wong,C.,
Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W.,
Theologis,A. and Ecker,J.R.
Arabidopsis ORF clones
Unpublished
TITLE Arabidopsis ORF clones
JOURNAL
REFERENCE 2 (bases 1 to 2013)
AUTHORS Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Carninci,P.,
Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T.,
Kamaya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lin,J., Miranda,M.,
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Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Wong,C.,
Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W.,
Theologis,A. and Ecker,J.R.
Direct Submission
Submitted (15-MAY-2003) Salk Institute Genomic Analysis Laboratory

```

(SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

COMMENT RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y., and Shinozaki, K.

The Salk, Stanford, PGECC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Bowser, L., Chan, M.M., Chang, C.M., Dale, J.M., Hsuan, V.W., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Davis, R.W., Theologis, A., and Ecker, J.R.

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

FEATURES

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ORGANISM Arabidopsis thaliana
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AUTHORS Southwick, A., Nguyen, M., Tripp, M., Palm, C.J., Jones, T., Wu, T., Carninci, P., Chen, H., Cheuk, R., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hayashizaki, Y., Hsuan, V.W., Lee, J.M., Ishida, J., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Onodera, C.S., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Shinn, P., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.
TITLE Direct Submission
JOURNAL Submitted (20-DEC-2002) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
COMMENT e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y., and Shinozaki, K.

The Salk, Stanford, PGECC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen, M., Tripp, M., Southwick, A., Palm, C.J., Jones, T., Wu, T., Chen, H., Cheuk, R., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.W., Lee, J.M., Kim, C.J., Quach, H.L., Onodera, C.S., Shinn, P., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Ecker, J., Theologis, A. and Davis, R.W.

Nguyen, M., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIs.

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ORIGIN

Query Match 5.5%; Score 93; DB 15; Length 2603;
Best Local Similarity 54.5%; Pred. No. 3.8e-08;
Matches 186; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 1116 GTGGCCCTTACTTGGCAGCAATGATGTCTTGTTCAGAAATTCAGGCGCGTGAGAA 1175
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QY 1176 TGTCTTGAAGGATACAAATTAAGCAATGCAATTCAGTTGCCAGTATTTGGCAGCGCT 1235
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DEFINITION

ACCESSION

VERSION

KEYWORDS

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ORGANISM

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

1 Totoki Y., Seki, M., Ishida, J., Nakajima, M., Enju, A., Kamiya, A.,
Narusaka, M., Shin-i, T., Nakagawa, M., Sakamoto, N., Oishi, K.,
Kohara, Y., Kobayashi, M., Toyoda, A., Sakaki, Y., Sakurai, T., Iida, K.,
Akiyama, K., Satou, M., Toyoda, T., Konagaya, A., Carninci, P.,
Kawai, J., Hayashizaki, Y. and Shinozaki, K.

TITLE

JOURNAL

REFERENCE

AUTHORS

2 (bases 1 to 1172)
Submitted (22-MAR-2005) Motoaki Seki, RIKEN Genomic Sciences
Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa,
230-0045, Japan (E-mail:mseki@gsc.riken.jp,
URL:http://range.gsc.riken.jp/, Tel:81-45-503-9625,
Fax:81-45-503-9586)
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al. (1998) Plant J. 15:707-720;
Seki et al. (2002) Science 296:141-145).

COMMENT

This clone is in a modified pBluescript vector.
Please visit our web site (<http://range.gsc.riken.jp/>) for further
details.

FEATURES

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Best Local Similarity 53.6%; Pred. No. 1.3e-07;
Matches 188; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

QY 1116 GTGGCCCTTACTTGGCAGCAATTCATGCTGTTTTCAGAAATTCAGGCGCGTGAGAA 1175
Db 696 GTTGCTCATTTACTTCCGAGCAGATGTTCTACGTAACAATCTCCAGGAGTTGGTGAA 755

QY 1176 TGTCTTGAAGGATACAAATTAAGCAATTCAGTTGCCAGTATTTGGCAGCGCT 1235
Db 756 ACATTCGGGAGAGTGACTATCGAAGCAATGGCTTATGGTCTTCCGGTGTCTGGAACAGAT 815

QY 1236 GCTGGAGGACCAACGAGATGCTCTGGACGGCTCGACTGGGCTTCTGCATCTCTGCTGG 1295
Db 816 GCTGGAGGAACAAAGAGATAGTGGAGCACAATGTTACAGGGCTACTTTCATCTCTGTTGGG 875

QY 1296 AAGGAGGGCGTGGCGCTCTTGCAAGAACATCGTCAGACTCGCAAGCACCAGCGAGCAG 1355
Db 876 AGGCAGAGTAACAAGTTTGGCAGAGATCTTTTGTCTTCTTAGAAACCATCTACA 935

QY 1356 AGGGTCTCCATGGGGGAAAAGGGCTATGCGAGGGTGAAGGAAATGTTTCATGGAGCACCAC 1415
Db 936 AGGCTACAACATAGGTAGCCAGGAGCTGAAATCGTTGAGAGATGTATCATGAAGCAGCAC 995

QY 1416 ATGGCTGAGAGATCGCGCGGTGTTGAAGGATGTCCTGAGGAATTCACAG 1466
Db 996 ATGTACAAGAGATTTGTGGATGTTCTTAGTCAAATGTATGAGACACTAACTG 1046

Search completed: March 17, 2006, 02:40:37
Job time : 8739 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 16, 2006, 23:50:12 ; Search time 1063 Seconds

(without alignments)
10671.032 Million cell updates/sec

Title: US-09-938-294-2

Perfect score: 1702

Sequence: 1 attcgctcgattgtatcc.....gaggagatttcaatcttagt 1702

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001as.*
- 5: Geneseq2001bs.*
- 6: Geneseq2002as.*
- 7: Geneseq2002bs.*
- 8: Geneseq2003as.*
- 9: Geneseq2003bs.*
- 10: Geneseq2003cs.*
- 11: Geneseq2003ds.*
- 12: Geneseq2004as.*
- 13: Geneseq2004bs.*
- 14: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1647	96.8	1647	13	ADX09132 Plant ful
2	589.6	34.6	1715	3	AAC42068 Arabidops
3	426.2	25.0	1094	13	ADR65394 Cotton cd
4	362	15.4	276	7	ADs71019 Corn seed
5	257	15.1	257	7	ADs71062 Corn seed
6	244.8	14.4	948	13	ADR62845 Cotton cd
7	233	13.7	583	10	ABX56781 Arabidops
8	227	13.3	625	13	ADR62846 Cotton cd
9	227	13.3	625	13	ACN58791 Cotton gy
10	210	12.3	382	13	ADR65395 Cotton cd
11	158.6	9.3	514	13	ACN58833 Cotton gy
12	154.6	9.1	284	3	AAA31140 Plant mic
13	74	4.3	1964	13	ADT18408 Plant cDN
14	67.4	4.0	254	9	ADA60128 Soybean s
15	67.4	4.0	254	12	ADQ06025 Soybean t
16	52.4	3.1	2387	8	ABT17892 Aspergill
17	52.4	3.1	3495	8	ABT19706 Aspergill
18	50.4	3.0	90597	10	ADJ72363 Streptomy
19	50.4	3.0	90600	6	ABQ78872 S. roseos

C	20	50	2.9	6997	10	ADD29793	Human tum
	21	49.8	2.9	912	3	AZ93717	HSV-1 V22
	22	49.2	2.9	1383	10	ADG33861	Actinomyc
	23	49	2.9	5877	6	ABS78681	Kitaseatos
	24	49	2.9	5877	14	ABE12658	Eneidiyne
	25	49	2.9	5877	14	AEC10251	Kitasatos
	26	48.6	2.9	872	13	ADX49110	Plant ful
	27	48.4	2.8	1076	2	AZ30007	Optimised
	28	48.4	2.8	1082	6	ABA92912	Organopho
	29	48.2	2.8	843	13	ADS15486	HSV-1 pol
	30	48.2	2.8	856	2	AZ19784	Herpes si
	31	48.2	2.8	856	2	AZ207807	HSV-1 teg
	32	48.2	2.8	900	3	AZ29395	HSV-1 VP2
	33	48.2	2.8	903	6	ABV73163	Herpes si
	34	48.2	2.8	903	12	ADK68679	Epitope 1
	35	48.2	2.8	903	12	ADQ10477	Herpes si
	36	48.2	2.8	903	13	ADS80957	Tumour as
	37	48.2	2.8	903	13	ADW76736	Human cyt
	38	48.2	2.8	906	13	ADS15488	HSV-1 pol
	39	48.2	2.8	912	2	AAX26227	HIV-1 VP2
	40	48.2	2.8	912	3	AZ88468	HSV-1 VP2
	41	48.2	2.8	912	4	AZF58996	HSV-1 VP2
	42	48.2	2.8	912	6	ABA93386	HSV-1 VP2
	43	48.2	2.8	912	10	ADF70996	Phosphope
	44	48.2	2.8	912	12	ADM83002	Transcell
	45	48.2	2.8	950	2	AAV17085	Herpes si

ALIGNMENTS

RESULT 1

ADX09132

ID ADX09132 standard; cDNA; 1647 BP.

XX AC ADX09132;

XX DT 21-APR-2005 (first entry)

XX DE Plant full length insert polynucleotide seqid 3707.

XX KW plant protectant; plant growth regulant; gene therapy; plant;

XX KW recombinant DNA construct; physical array; plant breeding marker;

XX KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

XX KW extreme osmotic condition; pathogen tolerance; pest tolerance;

XX KW growth rate; cell cycle pathway; disease resistance;

XX KW galactomannan production; lignin production; plant growth regulator;

XX KW yield; plant growth; plant development; seed oil; protein yield;

XX KW protein content; gene; ss.

XX OS Unidentified.

XX PN US2004034888-A1.

XX PD 19-FEB-2004.

XX PR 28-APR-2003; 2003US-00425114.

XX PR 06-MAY-1999; 99US-00304517.

XX PR 05-NOV-2001; 2001US-00985678.

XX (LIUJ/) LIU J.

XX (ZHOU/) ZHOU Y.

XX (KOVA/) KOVALIC D K.

XX (SCRE/) SCREEN S E.

XX (TABA/) TABASKA J E.

XX (CAOY/) CAO Y.

XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX DR WPI; 2004-180133/17.

XX PT New recombinant DNA construct, useful for improving plant tolerance to

PR	18-JUN-1999	99US-01394611
PR	18-JUN-1999	99US-0139462P
PR	18-JUN-1999	99US-0139463P
PR	18-JUN-1999	99US-0139750P
PR	18-JUN-1999	99US-0139763P
PR	21-JUN-1999	99US-0139817P
PR	21-JUN-1999	99US-0139899P
PR	22-JUN-1999	99US-0140033P
PR	23-JUN-1999	99US-0140354P
PR	24-JUN-1999	99US-0140695P
PR	28-JUN-1999	99US-0140823P
PR	29-JUN-1999	99US-0140991P
PR	30-JUN-1999	99US-0141287P
PR	01-JUL-1999	99US-0141842P
PR	01-JUL-1999	99US-0142154P
PR	02-JUL-1999	99US-0142055P
PR	06-JUL-1999	99US-0142390P
PR	08-JUL-1999	99US-0142803P
PR	09-JUL-1999	99US-0143202P
PR	12-JUL-1999	99US-0143977P
PR	13-JUL-1999	99US-0143542P
PR	14-JUL-1999	99US-0143624P
PR	15-JUL-1999	99US-0144005P
PR	16-JUL-1999	99US-0144085P
PR	16-JUL-1999	99US-0144086P
PR	19-JUL-1999	99US-0144325P
PR	19-JUL-1999	99US-0144331P
PR	19-JUL-1999	99US-0144332P
PR	20-JUL-1999	99US-0144333P
PR	19-JUL-1999	99US-0144334P
PR	19-JUL-1999	99US-0144335P
PR	20-JUL-1999	99US-0144352P
PR	20-JUL-1999	99US-0144632P
PR	20-JUL-1999	99US-0144684P
PR	21-JUL-1999	99US-0144814P
PR	21-JUL-1999	99US-0145086P
PR	21-JUL-1999	99US-0145088P
PR	22-JUL-1999	99US-0145085P
PR	22-JUL-1999	99US-0145087P
PR	22-JUL-1999	99US-0145089P
PR	23-JUL-1999	99US-0145192P
PR	23-JUL-1999	99US-0145145P
PR	23-JUL-1999	99US-0145218P
PR	23-JUL-1999	99US-0145224P
PR	26-JUL-1999	99US-0145276P
PR	27-JUL-1999	99US-0145913P
PR	27-JUL-1999	99US-0145918P
PR	27-JUL-1999	99US-0145951P
PR	28-JUL-1999	99US-0145951P
PR	02-AUG-1999	99US-0146386P
PR	02-AUG-1999	99US-0146388P
PR	02-AUG-1999	99US-0146389P
PR	02-AUG-1999	99US-0147038P
PR	04-AUG-1999	99US-0147204P
PR	04-AUG-1999	99US-0147302P
PR	05-AUG-1999	99US-0147192P
PR	05-AUG-1999	99US-0147260P
PR	06-AUG-1999	99US-0147303P
PR	06-AUG-1999	99US-0147416P
PR	09-AUG-1999	99US-0147493P
PR	09-AUG-1999	99US-0147935P
PR	10-AUG-1999	99US-0148171P
PR	11-AUG-1999	99US-0148319P
PR	12-AUG-1999	99US-0148341P
PR	13-AUG-1999	99US-0148565P
PR	13-AUG-1999	99US-0148684P
PR	16-AUG-1999	99US-0149368P
PR	17-AUG-1999	99US-0149175P
PR	18-AUG-1999	99US-0149426P
PR	20-AUG-1999	99US-0149722P
PR	20-AUG-1999	99US-0149723P
PR	22-AUG-1999	99US-0149929P
PR	23-AUG-1999	99US-0150902P

[illegible]

ID	ADR65394 standard; cDNA; 1094 BP.	Best Local Similarity 65.0%; Pred. No. 9e-110;	
XX	AC	Matches 666; Conservative 0; Mismatches 348; Indels 11; Gaps 2;	
XX	ADR65394;		
XX	02-DEC-2004 (first entry)		
XX	Cotton cDNA sequence, SEQ ID 6175.		
XX	Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;		
KW	drought tolerance; plant disease resistance; galactomannan; lignin;		
KW	plant growth regulator; heat tolerance; herbicide tolerance;		
KW	homologous recombination; extreme osmotic condition tolerance;		
KW	pathogen resistance; pest resistance; yield; photosynthesis; seed oil;		
KW	stress resistance.		
XX	Gossypium hirsutum.		
OS	US2004181830-A1.		
XX	16-SEP-2004.		
XX	29-JAN-2004; 2004US-00767795.		
XX	07-MAY-2001; 2001US-00849529.		
PR	12-DEC-2001; 2001US-00021323.		
XX	(KOVA/) KOVALIC D K.		
PA	(ZHOU/) ZHOU Y.		
PA	(CAOY/) CAO Y.		
XX	Kovalic DK, Zhou Y, Cao Y;		
PI	WPI; 2004-667718/65.		
XX	New recombinant nucleic acid molecules and polypeptides from Gossypium		
PT	hirsutum, useful for producing plants with improved biological		
PT	characteristics (e.g. improved plant cold or drought tolerance).		
XX	Claim 1; SEQ ID NO 6175; 14pp; English.		
XX	The invention relates to a recombinant polynucleotide comprising any of		
CC	the 58798 Cotton plant cDNA sequences mentioned in the specification.		
CC	Also a recombinant polypeptide comprising any of the 58798 amino acid		
CC	sequences mentioned in the specification and producing a plant having an		
CC	improved property. Producing a plant having an improved property		
CC	comprises transforming a plant with a recombinant construct comprising a		
CC	promoter region functional in a plant cell operably joined to a		
CC	polynucleotide comprising a coding sequence for a polypeptide associated		
CC	with the property, and growing the transformed plant. The polypeptide is		
CC	useful for improving plant cold tolerance, manipulating growth rate in		
CC	plant cells by modification of the cell cycle pathway, improving plant		
CC	drought tolerance, providing increased resistance to plant disease,		
CC	producing galactomannan (or lignin or plant growth regulators), improving		
CC	plant heat tolerance, improving plant tolerance to herbicides, increasing		
CC	the rate of homologous recombination in plants, improving plant tolerance		
CC	to extreme osmotic conditions or to pathogens or pests, improving yield		
CC	by modification of photosynthesis, modifying seed oil or protein yield		
CC	and/or content, improving yield by modification of carbohydrate, nitrogen		
CC	or phosphorus use and/or uptake, or improving yield by providing improved		
CC	plant growth and development under at least one stress condition. The		
CC	polynucleotide and polypeptide may also be used in recombinant DNA		
CC	constructs, in physical arrays of molecules, as plant breeding markers,		
CC	or in computer-based storage and analysis systems. The present sequence		
CC	is a Cotton plant cDNA of the invention. NOTE: The sequence data for this		
CC	patent did not form part of the printed specification, but was obtained		
CC	in electronic format directly from USPTO at		
CC	seqdata.uspto.gov/sequences.html?DocID=20040181830. However only 6585		
CC	polynucleotide sequences were available, the remaining 5213		
CC	polynucleotides and all 58798 protein sequences were not present.		
XX	Sequence 1094 BP; 335 A; 209 C; 258 G; 292 T; 0 U; 0 Other;		
XX	Query Match 25.0%; Score 426.2; DB 13; Length 1094;		

QY	627	ATGCGTGGGCATTTACTTTAAGCTTGAATATGTCAAAACATCTTCCCTTGTGTGCTGGAGCC	686
DB	13	ATGCGAGGCCATTTCTTTAAATTAGAGATATGAAGCATCGACGTCTGTATCTGTGCA	72
QY	687	ATGATTGATTCTCATACAAACGGCTGAGTATTGGAAATAGCA-----GGACTAGCGATCG	739
DB	73	ATGATTGATTACACAGCTCACAGCGGAAATATTGGAGAAATACCCACGCGCGCGCGCGCG	132
QY	740	CCTGAAATACAGATGCCAACAATTATGTTTTCACCTGGGATAGTAAAGAACTAAT	799
DB	133	GCCGAAGATTAAATGCGCTGAGACTATGTTTTCACCTTGGAAATAGCAATGAATGAT	192
QY	800	GGAAGTCTGCTGAAGACAATGTGCGAAGAGAGTCTCAGCGGAACATATTCTGTAATCCCT	859
DB	193	GCAAGTTCAGAGACAGCTGTGGCTAAAGGGTTTGGTGGAACATGTTCTGTAATCGCT	252
QY	860	TGGATACGGAGTGAGGATCTCTGTTTGCATTAATAACAGATGTATCACGAGGAAAGG	919
DB	253	TGGAGTGGCAATGACGATTTACTCTTTGCTTAAATAATAGTGTTCACGAGGAAAGG	312
QY	920	ACAAGACTTATTTCTTCAAGCAATTTTATCAGGCTTTGACGCTCATCCACACGAGAACT	979
DB	313	GCAGGATCTCTTTCTACGCGCTTTCTACGAGCGCTTACAACTGATCAAGCAAAAGAAAT	372
QY	980	TAAAGTCTGCTAGATACATGCTGTAGTTGTGGGAAGTGTATTAATGCTCAGACCAAAAT	1039
DB	373	GCAGGTGCCACCATTTGCATGCAATGTAATTTGGGAAGTGCATGAGTGGCATACGAACT	432
QY	1040	TGAGACTCAGTTTACGTGATCTTTTGGTGAAGAACACGATTCATGACCGTGTCCATTTGT	1099
DB	433	TGAATGGAATTTACGAGCTTATGTAAACACAGAGAAATTTCAAGATCGTGTTCATTTGT	492
QY	1100	GAAACAGACATTTGGCAGTGGCGCCCTTACTTGGCAGCAATTTGATGCTGTTTTCAGAAATC	1159
DB	493	GAACAAAACTCTTAAACAGTAGCTCCATATTTAGCTGCCGTAGATGTTTGTTCAGAAATC	552
QY	1160	TACGCGCGTGGAGAAATCTTTTGAAGGATACAAATGAAGCAATGGCAATTCAGTTGCC	1219
DB	553	TAGGAGCGGGAGAAATCTTTTGGAGCATTAACATCGAAGCAATGGCAATTCAGTTGCC	612
QY	1220	AGT-----ATTGGGACCGGCTGCTGGAGGAGCACCGAGATCGTCTCGACGCTCGACTG	1275
DB	613	TGTGCTGACAGGGAACAGCTGCCGGGGGACAAACGGAATAGTAGTGAACGCGCACAAAG	672
QY	1276	GCCTTCTGATCTCTGCGGAGGAGGCGGTGGCGCTCTTTCAGAAAGACATCGTCAGAC	1335
DB	673	GTTTATTGCACTCTGCGGAAAGAGGGGTGACAACTCTGGCGAAACATATTGTGAAC	732
QY	1336	TGCGAAGCCACGCGGAGCAGAGGGGTCTCCATGGGGGAAAGGGCTATGCGAGGGTGAAGG	1395
DB	733	TAGCTACGATGTAGAGAGAGGCTTCAATAGGAAGAGAGGGGTACGAAGGGTGAAG	792
QY	1396	AAATGTTTCATGGAGCACCACTATGGCTGAGAGGATCGCGCGGTGTGTAAGGATGCTCTGA	1455
DB	793	AAAGATTTCTAGAACATCACATGGCAGAGAGAAATTTGTTGAGTACTTAAAGAAGCGTTGA	852
QY	1456	GGAATACAGAGACACTCCAGGCTTTCAGCTTTCGCGTCCCATCAGCTTCGCGCTAAACA	1515
DB	853	GGAAGCTTAAATACAGATCAAGTAAACACCTTTTGACAGTGAACACCCCGCCACCATAA	912
QY	1516	TGTTGAACCTAGATTTTACGGGCTACGCTTACGCTGTGAGGTGTGTAACCTGTAGATTGA	1575
DB	913	AATTAACATAGGATATATCCAGTTTTCATTAATTAATGAGAGTACATCTTTAATCTCG	972
QY	1576	CTCTGTTGCTTACTTTTTTCAATTCATGTTTTTACCTATTTAGGCCCATGTCGATTTT	1635
DB	973	GCCTTTTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1032
QY	1636	CCAAAT 1640	

DB 1033 ACATT 1037

RESULT 4

ID ADS71019 standard; cDNA; 276 BP.

XX

AC ADS71019;

XX

XX 18-NOV-2004 (first entry)

DE

XX Corn seedling-derived polynucleotide (cpds), SEQ ID 6035.

DE

XX Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth;

KW seed development; disease resistance; insect infestation; fungal disease;

KW bacterial infection; Goss' Bacterial Wilt; blight;

KW Stewart's bacterial Wilt; Holcus spot; bacterial leaf blight; leaf spot;

KW bacterial stripe; maize dwarf mosaic virus infection;

KW environmental stress; water stress; pH stress; temperature stress;

KW pollution; injury; pesticide.

XX

OS Zea mays.

XX

XX US2003237110-A9.

XX

XX 25-DEC-2003.

XX

XX 06-AUG-2001; 2001US-00923876.

XX

XX 12-MAY-1998; 98US-0085331P.

PR 21-APR-1999; 99US-00298329.

XX

XX (INCY-) INCYTE PHARM INC.

XX

PI Lalgudi RV, Ito LY, Sherman BK;

XX

XX WPI; 2002-195165/25.

XX

XX New corn seedling-derived polynucleotides and polypeptides, useful in

PT identifying and altering desired characteristics associated with growth

PT and development, disease resistance, environmental adaptability, quality

PT and yield.

XX

XX Claim 3; SEQ ID NO 6035; 33pp; English.

XX

XX The invention relates to a corn seedling-derived polynucleotide (cdp)

CC selected from ADS64985-ADS71316, or their complements and fragments. Also

CC included are a composition for the detection of altered expression of a

CC cdp (comprising a polynucleotide selected from ADS64985-ADS71316), a

CC method of detecting a polynucleotide in a biological sample using a cdp,

CC a method for using oligomers (and amplification) to recover a regulatory

CC element from a DNA library using oligomers designed against a cdp, a

CC seedling specific regulatory element that regulates the expression of a

CC cdp, an expression vector containing a cdp or regulatory element, a plant

CC transformed with the vector, a host cell containing the vector (and

CC expressing a corn seedling derived protein, CDP), an anti-CDP antibody,

CC identifying a compound which binds a CDP and screening a plurality of

CC compounds for binding to cdp polynucleotide. The cdp polynucleotides,

CC proteins, vectors, cells and antibodies are useful for the

CC identification, evaluation and alteration of seed growth and development,

CC disease resistance (e.g. to insect infestation, fungal disease, bacterial

CC infection, Goss' Bacterial Wilt, blight, Stewart's bacterial Wilt, Holcus

CC spot, bacterial leaf blight, leaf spot, bacterial stripe and maize dwarf

CC mosaic virus infection) and resistance to environmental stress (e.g.

CC water stress, pH stress, temperature stress, pollution, injury or

CC pesticides. The present sequence is cdp cDNA sequence.

XX

SQ Sequence 276 BP; 64 A; 58 C; 83 G; 69 T; 0 U; 2 Other;

Query Match 15.4%; Score 262; DB 7; Length 276;

Best Local Similarity 99.3%; Pred. No. 1.6e-63;

Matches 273; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

1034 CAAATTTGAGACTCAGTTACGTGACTTTGTGTGAAGAACACGATTCATGACCGTGTCCA 1093

1 CAAATTTGAGACTCAGTTACGTGACTTTGTGTGAAGAACACGATTCATGACCGTGTCCA 60

1094 TTTTGTGAACAAGACATTGGCAGTGGCCCTTACTTTGGCAGCAATTGATGCTGTGTCCA 1153

61 TTTTGTGAACAAGACATTGGCAGTGGCCCTTACTTTGGCAGCAATTGATGCTGTGTCCA 120

1154 GAAATTTCTCAGGGCCGTGGAGAAATGCTTTTGGAGAGGATAACAATTGAAGCAATGGCATTCAA 1213

121 GAAATTTCTCAGGGCCGTGGAGAAATGCTTTTGGAGAGGATAACAATTGAAGCAATGGCATTCAA 180

1214 GTTGGCAGTATTGGGACGCGTCTGCGAGGACACGAGATCGTCTGGACGGTCTGAC 1273

181 GTTGGCAGTATTGGGACGCGTCTGCGAGGACACGAGATCGTCTGGACGGTCTGAC 240

1274 TGGCCTTTCTGCATCTCTGCGAAGAGGGCGGTGG 1308

241 TGGCC-TCTGCATCTCTGCGAAGAGGGCGGTGG 274

RESULT 5

ADS71062

ID ADS71062 standard; cDNA; 257 BP.

XX

XX ADS71062;

XX

DT 18-NOV-2004 (first entry)

XX

DE Corn seedling-derived polynucleotide (cpds), SEQ ID 6078.

DE

XX Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth;

KW seed development; disease resistance; insect infestation; fungal disease;

KW bacterial infection; Goss' Bacterial Wilt; blight;

KW Stewart's bacterial Wilt; Holcus spot; bacterial leaf blight; leaf spot;

KW bacterial stripe; maize dwarf mosaic virus infection;

KW environmental stress; water stress; pH stress; temperature stress;

KW pollution; injury; pesticide.

XX

OS Zea mays.

XX

XX US2003237110-A9.

XX

XX 25-DEC-2003.

XX

XX 06-AUG-2001; 2001US-00923876.

XX

XX 12-MAY-1998; 98US-0085331P.

PR 21-APR-1999; 99US-00298329.

XX

XX (INCY-) INCYTE PHARM INC.

XX

PI Lalgudi RV, Ito LY, Sherman BK;

XX

XX WPI; 2002-195165/25.

XX

XX New corn seedling-derived polynucleotides and polypeptides, useful in

PT identifying and altering desired characteristics associated with growth

PT and development, disease resistance, environmental adaptability, quality

PT and yield.

XX

XX Claim 3; SEQ ID NO 6078; 33pp; English.

XX

XX The invention relates to a corn seedling-derived polynucleotide (cdp)

CC selected from ADS64985-ADS71316, or their complements and fragments. Also

CC included are a composition for the detection of altered expression of a

CC cdp (comprising a polynucleotide selected from ADS64985-ADS71316), a

CC method of detecting a polynucleotide in a biological sample using a cdp,

CC a method for using oligomers (and amplification) to recover a regulatory

CC element from a DNA library using oligomers designed against a cdp, a

CC seedling specific regulatory element that regulates the expression of a

CC cdp, an expression vector containing a cdp or regulatory element, a plant

CC transformed with the vector, a host cell containing the vector (and

CC expressing a corn seedling derived protein, CDP), an anti-CDP antibody,

CC identifying a compound which binds a CDP and screening a plurality of

CC compounds for binding to cdp polynucleotide. The cdp polynucleotides,

CC proteins, vectors, cells and antibodies are useful for the

CC identification, evaluation and alteration of seed growth and development,

CC disease resistance (e.g. to insect infestation, fungal disease, bacterial

CC infection, Goss' Bacterial Wilt, blight, Stewart's bacterial Wilt, Holcus

CC spot, bacterial leaf blight, leaf spot, bacterial stripe and maize dwarf

CC mosaic virus infection) and resistance to environmental stress (e.g.

CC water stress, pH stress, temperature stress, pollution, injury or

CC pesticides. The present sequence is cdp cDNA sequence.

XX

SQ Sequence 276 BP; 64 A; 58 C; 83 G; 69 T; 0 U; 2 Other;

Query Match 15.4%; Score 262; DB 7; Length 276;

Best Local Similarity 99.3%; Pred. No. 1.6e-63;

Matches 273; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

CC expressing a corn seedling derived protein, CDP), an anti-CDP antibody,
 CC identifying a compound which binds a CDP and screening a plurality of
 CC compounds for binding to cdp polynucleotide. The cdp polynucleotides,
 CC proteins, vectors, cells and antibodies are useful for the
 CC identification, evaluation and alteration of seed growth and development,
 CC disease resistance (e.g. to insect infestation, fungal disease, bacterial
 CC infection, Goss' Bacterial Wilt, blight, Stewart's bacterial wilt, Holcus
 CC spot, bacterial leaf blight, leaf spot, bacterial stripe and maize dwarf
 CC mosaic virus infection) and resistance to environmental stress (e.g.
 CC water stress, pH stress, temperature stress, pollution, injury or
 CC pesticides. The present sequence is cdp cDNA sequence.

XX Sequence 257 BP; 61 A; 55 C; 73 G; 68 T; 0 U; 0 Other;

Query Match 15.1%; Score 257; DB 7; Length 257;

Best Local Similarity 100.0%; Pred. No. 4e-62;

Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1035 AAATTGAGACTCAGTACGTTGTTGGTGAAGAACACGATTCATGACCGTGTCCAT 1094

DB 1 AAATTGAGACTCAGTACGTTGTTGGTGAAGAACACGATTCATGACCGTGTCCAT 60

QY 1095 TTTGTGAACAAGACATTTGGCAGTGGCCCTTACTTGGCAGCAATGATGCTGTTCAG 1154

DB 61 TTTGTGAACAAGACATTTGGCAGTGGCCCTTACTTGGCAGCAATGATGCTGTTCAG 120

QY 1155 AATTCTCAGGCGGTGGAGATGCTTTGAAGATAAACAAATGAAGCAATGCAATCAAG 1214

DB 121 AATTCTCAGGCGGTGGAGATGCTTTGAAGATAAACAAATGAAGCAATGCAATCAAG 180

QY 1215 TTGCCAGTATTGGCAGCGCTGCTGGAGGACACGAGATCGTCTTGACCGGCTCGACT 1274

DB 181 TTGCCAGTATTGGCAGCGCTGCTGGAGGACACGAGATCGTCTTGACCGGCTCGACT 240

QY 1275 GGCCTTCTCATCTCTGC 1291

DB 241 GGCCTTCTCATCTCTGC 257

RESULT 6

ADR62845

ID ADR62845 standard; cDNA; 948 BP.

XX

AC ADR62845;

DT 02-DEC-2004 (first entry)

XX

DE Cotton cDNA sequence, SEQ ID 3626.

XX

KW Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;
 KW drought tolerance; plant disease resistance; galactomannan; lignin;
 KW plant growth regulator; heat tolerance; herbicide tolerance;
 KW homologous recombination; extreme osmotic condition tolerance;
 KW pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
 KW stress resistance.

XX Gossypium hirsutum.

OS

XX US2004181830-A1.

PN

XX 16-SEP-2004.

PD

XX 29-JAN-2004; 2004US-00767795.

PP

XX 07-MAY-2001; 2001US-00849529.

PR

XX 12-DEC-2001; 2001US-00021323.

XX

PA (KOVA/) KOVALIC D K.

PA (ZHOU/) ZHOU Y.

PA (CAOY/) CAO Y.

XX

PI Kovalic DK, Zhou Y, Cao Y;

XX

DR

XX

PT

PT

PT

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PS

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CC

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CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

Query Match

Best Local Similarity

Matches 352;

Conservative

Mismatches

Indels

Gaps

1;

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

WPI; 2004-667718/65.

New recombinant nucleic acid molecules and polypeptides from Gossypium
 hirsutum, useful for producing plants with improved biological
 characteristics (e.g. improved plant cold or drought tolerance).

Claim 1; SEQ ID NO 3626; 14pp; English.

The invention relates to a recombinant polynucleotide comprising any of
 the 58798 Cotton plant cDNA sequences mentioned in the specification.
 Also a recombinant polypeptide comprising any of the 58798 amino acid
 sequences mentioned in the specification and producing a plant having an
 improved property. Producing a plant having an improved property
 comprises transforming a plant with a recombinant construct comprising a
 promoter region functional in a plant cell operably joined to a
 polynucleotide comprising a coding sequence for a polypeptide associated
 with the property, and growing the transformed plant. The polypeptide is
 useful for improving plant cold tolerance, manipulating growth rate in
 plant cells by modification of the cell cycle pathway, improving plant
 drought tolerance, providing increased resistance to plant disease,
 producing galactomannan (or lignin or plant growth regulators), improving
 plant heat tolerance, improving plant tolerance to herbicides, increasing
 the rate of homologous recombination in plants, improving plant tolerance
 to extreme osmotic conditions or to pathogens or pests, improving yield
 by modification of photosynthesis, modifying seed oil or protein yield
 and/or content, improving yield by modification of carbohydrate, nitrogen
 or phosphorus use and/or uptake, or improving yield by providing improved
 plant growth and development under at least one stress condition. The
 polynucleotide and polypeptide may also be used in recombinant DNA
 constructs, in physical arrays of molecules, as plant breeding markers,
 or in computer-based storage and analysis systems. The present sequence
 is a Cotton plant cDNA of the invention. NOTE: The sequence data for this
 patent did not form part of the printed specification, but was obtained
 in electronic format directly from USPTO at
 seqdata.uspto.gov/sequence.html?DocID=20040181830. However only 6585
 polynucleotide sequences were available, the remaining 52113
 polynucleotides and all 58798 protein sequences were not present.

Sequence 948 BP; 242 A; 195 C; 220 G; 291 T; 0 U; 0 Other;

Query Match 14.4%; Score 244.8; DB 13; Length 948;

Best Local Similarity 68.8%; Pred. No. 2.5e-58;

Matches 352; Conservative 0; Mismatches 157; Indels 3; Gaps 1;

QY 249 ACCGCGCTGCGCAGCGGAGTCCCTCGGGTTTCATGAGTCCCAAGTCGTGCTCTCGTC 308

DB 393 ATCGCGGCTGTGAAGCCGAGTCGGCTAGCTTTATGAGTCCACGGCTCGCTGGTT 452

QY 309 TCCCATGAGCTCTCCCTCTCTGGTGGTCCACTTTTACTGATGGAATTAGCATTTCTCTG 368

DB 453 TCGCACGAGCTCTCGCTTTCTGGTGGACCATTTGTTGGGATGGAGCTGGCATTCCTATTA 512

QY 369 AGGCATGTTGGCTCCCAAGTGGTGGATACCAACACGAGATCAACAAGAAATGAT 428

DB 513 AGAAGTGTGGTGGTGAAGTTTATGGATGCAATATGAAACCATCTCTGAAACAGATGA 572

QY 429 GTCACATATAGCTTGGAGCATAGGATGTTGAACCATGAGTGCAGGTTTACCAGCTAGA 488

DB 573 GTAACATATAGTTTGAACATAGATGTTGGACAGAGGATGACAGTTATCTCAGCTAAG 632

QY 489 GCACAGGAGGAGTTGATATGCTCTAAAGCTGATCTGTTTATCTTAAACACTGCTGTT 548

DB 633 GGGAAAGAGCTTTAGATCTCTCTAGAGCTGATTTGGTGTGTTTGAACACTGCTGATTT 692

QY 549 GCTGCAAGTGGCTTGACCCCTGTTCTGAAGATCATGTTCTTAAAGTCTTCCGAGATT 608

DB 693 GCTGGAAATGGCTGGATGTTGTTCTTAAGGAGATGTTTCATCGTGTCTTGCTTAAGG 752

QY 609 TTGTGTTGATCCATGAAATGGTGGCATTACTTTTAAGTTTGAATATCTCAAAACATCTT 668

DB 753 TTGTGTTGATCCATGAAATGGTGGCATTACTTTTAAGTTTGAATATCTCAAAACATCTT 812

QY 669 CCCTTTGT---TGCTGGAGCCCATGATGATTCTCTACAAACGGCTGAGTATTGGAATAGC 725

Db 813 TCCTCTTTGATCTGCTATGATTTGATTCCTCCATGTTACACAGAACTGGAGAT 872
 QY 726 AGGACTAGGATCGCTGAAATACAGATGCC 757
 Db 873 AGTACTAAAGACGTTTGAAGTTTAAATGTC 904

RESULT 7
 ABX56781/c
 ID ABX56781 standard; DNA; 583 BP.
 XX
 AC ABX56781;
 XX
 DT 20-FEB-2003 (first entry)
 XX
 DE Arabidopsis thaliana polynucleotide #133.
 XX
 KW Thale cress; gene; ds; genetic manipulation; plant; biosynthesis;
 KW genetic modification; environmental stress; disease resistance;
 KW fungicide; insecticide; stress tolerance.
 XX
 OS Arabidopsis thaliana.
 XX
 PN US2002040489-A1.
 XX
 PD 04-APR-2002.
 XX
 PF 26-JAN-2001; 2001US-00770152.
 XX
 PR 27-JAN-2000; 2000US-0178503P.
 XX

PA (GORL/) GORLACH J.
 PA (ANY/) AN Y.
 PA (HAM/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUY/) YU Y.
 PA (NAME/) NAMEKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 XX
 PI Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
 PI Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
 PI Hurban P;
 XX
 WPI; 2003-110410/10.

Novel Arabidopsis thaliana nucleic acid useful for identifying homologous or related genes, and to create genetically modified and transgenic organisms, such as plant cells and plants.
 Claim 1; SEQ ID NO 133; 45pp; English.
 The invention relates to Arabidopsis thaliana nucleic acid sequences. The DNA sequences and the polypeptides they encode are useful for identifying homologous or related genes, for producing compositions that modulate the expression or function of the polypeptides, for mapping functional regions of the protein, in diagnosis, for studying associated physiological pathways, for genetic manipulation of cells, preferably plant cells, in screening assays of various plant strains to determine the strains that are capable of withstanding a particular disease or

environmental stress, for enhancing or inhibiting production of biosynthetic products in plants and to create genetically modified and transgenic organisms, such as plant cells and plants. Transgenic plants are useful for introducing or improving disease resistance and stress tolerance in plants, screening biologically active agents, such as fungicides and insecticides, and for elucidating biochemical pathways. Sequences ABX56649-ABX57647 represent Arabidopsis thaliana polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 583 BP; 136 A; 141 C; 108 G; 198 T; 0 U; 0 Other;
 Query Match 13.7%; Score 233; DB 10; Length 583;
 Best Local Similarity 66.3%; Pred. No. 4.2e-55;
 Matches 335; Conservative 0; Mismatches 170; Indels 0; Gaps 0;
 QY 963 ATCCACACGAGAAACTTAAAGTCCTAGAAATACATGCTGTAGTTGTGGAAAGTATGTT 1022
 Db 568 ATCAAAGAGAGAAACTTCAGGTACCAACAATGCATGCAGTAGTAGTAGGACGACATG 509
 QY 1023 AATGCTCAGACCAAAATTTGAGACTCAGTTACGTGACTTTGTGTGTAAGAACAGATTAT 1082
 Db 508 AGCAAGACGACAAAGTTTCGAGACAGAGCTACGCAACTTTTGTCCGAGAAAGAACTTGAG 449
 QY 1083 GACCGTGCTCATTTTGTGAACAAGACATTTGGCAGTGGCCCTTACTTTGGCAGCAATTGAT 1142
 Db 448 AACTTTGTCCACTTCGTCAACAAACTCTAACCGTAGCACCATATATAGACCATAGAC 389
 QY 1143 GTGCTTGTTCAGAAATTTCTCAGGGCGGTGGAGAAATGCTTTGGAAAGGATACAAATTGAAGCA 1202
 Db 388 GTTCTTGTCCAAACTCCCAAGCCAGAGGAGATGCTTTGGGAGATATACATCGAAGCC 329
 QY 1203 ATGGCAATCAAGTTGCCAGTATTTGGCAGCGTCTGTGAGGAGCACCGAGATCGTCCTG 1262
 Db 328 ATGGCCTTTAAGCTACTTGTGTAATGCTGAGCGGAGGAAACAATGAGATTTGTAGTG 269
 QY 1263 GACGCTCGACTGGCTTCTGCATCTCTGGAGAGGGCGTGGCGCTCTTTCGCAAG 1322
 Db 268 AATGGAACGACTGGTCTGTATCATAGTCGAGGAAAGAGGAGTATACCTCTCGCCAAG 209
 QY 1323 AACATCGTCAGACTCGCAAGCCACGCGAGCAGAGGGTCTCCATGGGGGAAAGGGCTAT 1382
 Db 208 AACATAGTGAAGTTGGCGAGCAAGTTGAGTTACGGCTGAGATGGGAAATAATGGGTAT 149
 QY 1383 GGCAGGGTGAAGAAATGTTTCATGGAGCACCATGCTGGCTGAGAGGATCCGGGGGTGTG 1442
 Db 148 GAGAGAGTAAAGAGATGTTTTTGGAAACATCATATGTCAATCGAATAGCTTCGGGTACTC 89
 QY 1443 AAGGATGCTCTGAGGAATTCACAGG 1467
 Db 88 AAAGAAGTCTTTCGAACACGCAAAAGG 64
 RESULT 8
 ADR62846
 ID ADR62846 standard; cDNA; 625 BP.
 XX
 AC ADR62846;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Cotton cDNA sequence, SEQ ID 3627.
 XX
 KW Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;
 KW drought tolerance; plant disease resistance; galactomannan; lignin;
 KW plant growth regulator; heat tolerance; herbicide tolerance;
 KW homologous recombination; extreme osmotic condition tolerance;
 KW pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
 KW stress resistance.
 XX
 OS Gossypium hirsutum.
 XX

PN US2004181830-A1.
 XX 16-SEP-2004.
 XX 29-JAN-2004; 2004US-00767795.
 XX 07-MAY-2001; 2001US-00849529.
 PR 12-DEC-2001; 2001US-00021323.
 XX (KOVA/) KOVALIC D K.
 PA (ZHOU/) ZHOU Y.
 PA (CAO/) CAO Y.
 XX Kovalic DK, Zhou Y, Cao Y;
 XX WPI; 2004-567718/65.
 XX New recombinant nucleic acid molecules and polypeptides from *Gossypium*
 PT hirsutum, useful for producing plants with improved biological
 PT characteristics (e.g. improved plant cold or drought tolerance).
 XX
 PS Claim 1; SEQ ID NO 3627; 14pp; English.
 XX The invention relates to a recombinant polynucleotide comprising any of
 CC the 58798 Cotton plant cDNA sequences mentioned in the specification.
 CC Also a recombinant polypeptide comprising any of the 58798 amino acid
 CC sequences mentioned in the specification and producing a plant having an
 CC improved property. Producing a plant having an improved property
 CC comprises transforming a plant with a recombinant construct comprising a
 CC promoter region functional in a plant cell operably joined to a
 CC polynucleotide comprising a coding sequence for a polypeptide associated
 CC with the property, and growing the transformed plant. The polypeptide is
 CC useful for improving plant cold tolerance, manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, improving plant
 CC drought tolerance, providing increased resistance to plant disease,
 CC producing galactomannan (or lignin or plant growth regulators), improving
 CC plant heat tolerance, improving plant tolerance to herbicides, increasing
 CC the rate of homologous recombination in plants, improving plant tolerance
 CC to extreme osmotic conditions or to pathogens or pests, improving yield
 CC by modification of photosynthesis, modifying seed oil or protein yield
 CC and/or content, improving yield by modification of carbohydrate, nitrogen
 CC or phosphorus use and/or uptake, or improving yield by providing improved
 CC plant growth and development under at least one stress condition. The
 CC polynucleotide and polypeptide may also be used in recombinant DNA
 CC constructs, in physical arrays of molecules, as plant breeding markers,
 CC or in computer-based storage and analysis systems. The present sequence
 CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20040181830. However only 6585
 CC polynucleotide sequences were available, the remaining 52213
 CC polynucleotides and all 58798 protein sequences were not present.
 XX
 SQ Sequence 625 BP; 144 A; 134 C; 158 G; 189 T; 0 U; 0 Other;
 Query Match 13.3%; Score 227; DB 13; Length 625;
 Best Local Similarity 70.7%; Pred. No. 2.2e-53;
 Matches 302; Conservative 0; Mismatches 125; Indels 0; Gaps 0;
 QY 240 GCCCTCAACACCGCGTCCGAGCGGAGTCCCTCGGTTTCATGAGTCCAAAGTCGCG 299
 DB 199 GCCCGCGAGATCGTCTGCAAGCGGAGTCCACTCAGTTTCATGAAAGTCCAAAGATTGT 258
 QY 300 CTCCTCGTCTCCATGAGTCTCCCTCTCTGTTGTCACACTTTTACTGATGAATAGCA 359
 DB 259 CTACTGGTGTGCACGAGTCTCGCTTTCTGTGTGACCACTTTGTGTGAGGTAGCA 318
 QY 360 TTCTCTTCTGAGCATGTTGGCTCGCAAGTGTGTGATACAAACACAGATACACAGAA 419
 DB 319 TTCTCTTAAAGAGTGTGTGCTGAGTTAATTTGGTTTACATTTATGAACCATCTGAA 378
 QY 420 ACAATATGATGCACATATAGCTTGGAGCAGATAGATGTTGAACCATGAGTGCAGTTTAA 479

DB 379 ACTGATGAAGTAATATATATAGTTTGAACATAAGATGTTGGACAGAGGAGTGCAGGTTTTC 438
 QY 480 CCAGCTTAGAGGACAGGAGGACGTTGATATTGCTCTAAAAGCTGATCTGGTTATCTTAAAC 539
 DB 439 TCCGGTTTGGAAAGAGCTATAGATCTGCTCTAAGAGCTGATTTGGTTGTTTGAAC 498
 QY 540 ACTGCTGTGCTGGCAAGTGGCTTCAACCTGTTCTTGAAGATCATGTTCTCTAAAGTCCTT 599
 DB 499 ACAGCGGTTGCTGGGAATGGGTAGATTATGTTCTTAAAGGAAGATATTCACCGTGTCTG 558
 QY 600 CCGAAGATTTTGTGCTGGATCCATCAATGCGTGGGCATTACTTTAAGTTGATATGTC 659
 DB 559 CCTAAGGTGTTGTGTTGGATCCATGAAATGCGAGGCCATTACTTCAATTAGAGTATGTA 618
 QY 660 AAACATC 666
 DB 619 AAGCATC 625
 RESULT 9
 ACN58791
 ID ACN58791 standard; cDNA; 625 BP.
 XX ACN58791;
 AC ACN58791;
 XX 02-DEC-2004 (first entry)
 DT 02-DEC-2004
 XX Cotton *Gossypium* tissue EST Clone ID: LIB3829-012-Q6-K6-G10, SEQ:13572.
 DE Cotton; plant; EST; expressed sequence tag; transgenic plant; *Gossypium*;
 XX variety Nuotot33B; library LIB3829; molecular tag; molecular marker;
 KW genetic mapping; molecular mapping; seed germination; plant growth;
 KW plant quality; plant yield; plant breeding; tissue printing; ss.
 XX *Gossypium hirsutum*.
 OS US2004123340-A1.
 PN 24-JUN-2004.
 XX 12-DEC-2001; 2001US-00021323.
 XX 14-DEC-2000; 2000US-0255619P.
 PR (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 XX Deikman J, Feng PCC, Fincher KL, Ziegler TE;
 XX WPI; 2004-479808/45.
 DR New isolated nucleic acid molecule that encodes a plant protein or its
 XX fragment, useful for isolating a variety of agronomically significant
 PT genes associated with plant growth, quality or yield, and as molecular
 PT tags to map genes.
 XX Claim 1; SEQ ID NO 13572; 34pp; English.
 PS The invention relates to 17880 cotton expressed sequence tags (ESTs;
 CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated
 CC from primed or non-primed seeds from variety DP50B, mature seeds from
 CC variety Coker 312 Beeswell 96 field, and androecium tissue, *Gossypium*
 CC tissue, developing fibres, carpal walls and septa from variety
 CC Nuotot33B. The invention also relates to substantially purified
 CC proteins or their fragments encoded by nucleic acid molecules of the
 CC invention, and to transformed plants having a nucleic acid construct
 CC comprising a nucleic acid of the invention. The cotton ESTs are useful as
 CC molecular tags to isolate genetic regions, to isolate genes, to map
 CC genes, to determine gene function and to determining whether genes are
 CC members of a particular gene family. The nucleic acid molecules may be
 CC used for isolating a variety of agronomically significant genes

CC associated with plant growth, quality, yield, and could also serve as
 CC links in metabolic and catabolic pathways. The nucleic acid molecules are
 CC also useful for identifying genes important in initiating and maintaining
 CC seed germination or that may be used to mitigate stresses encountered
 CC during seed germination. The ESTs additionally enable the acquisition of
 CC promoters and cis-regulatory elements which will be useful to express
 CC agronomically significant genes in these tissues and/or other tissues,
 CC and also permits the acquisition of molecular markers useful in breeding
 CC schemes, genetic and molecular mapping, and in cloning of agronomically
 CC significant genes. The nucleic acid molecules are further useful for
 CC detecting the expression level or pattern of a protein or mRNA and for
 CC detecting the presence or quantity of a protein by tissue printing. The
 CC present sequence represents a specifically claimed EST isolated from a
 CC cotton variety Nucleon338 gynoecium tissue cDNA library (L1B3829). The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the US
 CC patent office at seqdata.uspto.gov/sequence.html?DocID=US20040123340
 XX
 XX
 SQ Sequence 625 BP; 144 A; 134 C; 158 G; 189 T; 0 U; 0 Other;

Query Match 13.3%; Score 227; DB 13; Length 625;
 Best Local Similarity 70.7%; Pred. No. 2.2e-53;
 Matches 302; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 240 GCCTCAACACCGCGTCCAGCGGAGTCCCTCGGCTTCATGAGTCCAGCTCGG 299
 DB |||||
 QY 199 GCCCGCCAGATCGCTCTGCAAGCGAGTCCACTCAGTTTCATGAAGTCCAGATGTT 258
 DB |||||
 QY 300 CTCCTCGTCCCATGAGCTCCCTCTCTGGTGGTCCACTTTTACTGATGGAATAGCA 359
 DB |||||
 QY 259 CTACTGCTGCGCAGAGCTCTGCTTTCTGGTGGACCATTTGTTGATGGAGTAGCA 318
 DB |||||
 QY 360 TTTCTTCTGAGGCAATTTGGCTCGCAAGTGGTGTGATGAACAAACAGAGATCACAAGAA 419
 DB |||||
 QY 319 TTTCTATTAAAGAGTGTGGTCTGAAGTTAATGGGTACATTTATGAACCATCTGAA 378
 DB |||||
 QY 420 ACAATGATGTCATATAGCTGGAGCATAGATGTTGAACCATGGAGTGGAGGTTTGA 479
 DB |||||
 QY 379 ACTGATGAAGTATATATAGTTTAGAACATAGATGTTGGACAGAGAGTGGAGGTTTC 438
 DB |||||
 QY 480 CCAGCTTAGAGGACAGGAGGAGTGTATTTGCTCTAAAGCTGATCTGGTTATCTTAAAC 539
 DB |||||
 QY 439 TCGCGCTTTGAAAGAGCTATAGATCTGCTTAAGAGCTGATTTGGTTGTTTGAAC 498
 DB |||||
 QY 540 ATGCTGTTGCTGGCAAGTGGTGGTACCTGTTCTGAAAGATCATGTTCTTAAAGTCTT 599
 DB |||||
 QY 499 ACAGCGTGTCTGGGAAATGGGTAGATTTATGTTCTTAAAGAGATATTCACCGTGTCTG 558
 DB |||||
 QY 600 CCGAAGATTTGTTGGTCCATGAATCCGTTGGCATTTACTTTAAGTTGATATGTC 659
 DB |||||
 QY 559 CCTAAGGTGTTGGTGGATCCATGAATCCGAGGCCATTACTTCAATTTAGAGTATGTA 618
 DB |||||
 QY 660 AAACATC 666
 DB |||||
 QY 619 AAGCATC 625

RESULT 10
 ADR65395
 ID ADR65395 standard; cDNA; 382 BP.
 XX
 AC ADR65395;
 DT 02-DEC-2004 (first entry)
 XX
 DE Cotton cDNA sequence, SEQ ID 6176.
 XX
 KW Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;
 KW drought tolerance; plant disease resistance; galactomanan; lignin;
 KW plant growth regulator; heat tolerance; herbicide tolerance;
 KW homologous recombination; extreme osmotic condition tolerance;
 KW pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
 KW stress resistance.

XX Gossypium hirsutum.
 OS
 XX US2004181830-A1.
 FN
 XX 16-SEP-2004.
 PD
 XX 29-JAN-2004; 2004US-00767795.
 PF
 XX 07-MAY-2001; 2001US-00849529.
 PR
 XX 12-DEC-2001; 2001US-00021323.
 PR
 XX (KOVA/) KOVALIC D K.
 PA (ZHOU/) ZHOU Y.
 PA (CAOY/) CAO Y.
 XX
 XX Kovalic DK, Zhou Y, Cao Y;
 PI
 XX WPI; 2004-667718/65.
 DR
 XX
 XX New recombinant nucleic acid molecules and polypeptides from Gossypium
 PT hirsutum, useful for producing plants with improved biological
 PT characteristics (e.g. improved plant cold or drought tolerance).
 PT
 XX Claim 1; SEQ ID NO 6176; 14pp; English.
 PS
 XX The invention relates to a recombinant polynucleotide comprising any of
 CC the 58798 Cotton plant cDNA sequences mentioned in the specification.
 CC Also a recombinant polypeptide comprising any of the 58798 amino acid
 CC sequences mentioned in the specification and producing a plant having an
 CC improved property. Producing a plant having an improved property
 CC comprises transforming a plant with a recombinant construct comprising a
 CC promoter region functional in a plant cell operably joined to a
 CC polynucleotide comprising a coding sequence for a polypeptide associated
 CC with the property, and growing the transformed plant. The polypeptide is
 CC useful for improving plant cold tolerance, manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, improving plant
 CC drought tolerance, providing increased resistance to plant disease,
 CC producing galactomanan (or lignin or plant growth regulators), improving
 CC plant heat tolerance, improving plant tolerance to herbicides, increasing
 CC the rate of homologous recombination in plants, improving plant tolerance
 CC to extreme osmotic conditions or to pathogens or pests, improving yield
 CC by modification of photosynthesis, modifying seed oil or protein yield
 CC and/or content, improving yield by modification of carbohydrate, nitrogen
 CC or phosphorus use and/or uptake, or improving yield by providing improved
 CC plant growth and development under at least one stress condition. The
 CC polynucleotide and polypeptide may also be used in recombinant DNA
 CC constructs, in physical arrays of molecules, as plant breeding markers,
 CC or in computer-based storage and analysis systems. The present sequence
 CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20040181830. However only 6585
 CC polynucleotide sequences were available, the remaining 52213
 CC polynucleotides and all 58798 protein sequences were not present.
 XX
 XX Sequence 382 BP; 112 A; 76 C; 94 G; 100 T; 0 U; 0 Other;

Query Match 12.3%; Score 210; DB 13; Length 382;
 Best Local Similarity 73.8%; Pred. No. 1.1e-48;
 Matches 267; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 627 ATGCGTGGCATTTACTTTAAGTTGATATGTCACACATCTCCCTTTGTTGGAGCC 686
 DB |||||
 QY 13 ATGCGAGGCCATTTCTTCAAAATTAGATGATGAAGCATCGGCCGCTCTAGCTGGTGA 72
 DB |||||
 QY 687 ATGATTGATTCTCATACAACGGCTGAGTATTGGAATAGCAGGACTAGCCATCGCTGAAA 746
 DB |||||
 QY 73 ATGATTGATTTCACGCTCACGCGGATATTGGAAGATAGGACTCAAGAGCGTTGAAG 132
 DB |||||
 QY 747 ATACAGATGCCCAAACTTATTTGTTCTACCTGGGGAATAGTAAGAACTAATGGAATT 806
 DB |||||
 QY 133 ATTAAATGCTGAGACCTATGTTTTCACCTTGGAAATAGCAATGAATGATGCAAGTT 192
 DB |||||

QY 807 GCTGAAGACAATGTCGCAAGAGAGTCCTACGGAAACATATTCGTGAATCCCTTGGAGTA 866
 |||||
 Db 193 GCAGAGACAGTGTGCTAAAGGTTTTCGCGTGAACATTCGTGATCGCTTGGAGTG 252
 |||||
 QY 867 CGGAGTGAAGATCTCTGTTGCAATATAAACAAGTATACAGAGGAAAGGACAGAC 926
 |||||
 Db 253 CGCAATGACGATTTACTCTTTCGCTTAATAAATAGTGTTCACGAGGAAAGGCGCAGAT 312
 |||||
 QY 927 TTATTTCTTCAAGCATTTTATCAGGCTTTCAGGCTCATCAACACGAGAACTTAAAGTG 986
 |||||
 Db 313 CTCTTTCTAGCGCTTTCACGAGGCTTACAACTGATCAAGCAAAAGAAATGCAAGTG 372
 |||||
 QY 987 CC 988
 ||
 Db 373 CC 374

RESULT 11
 ACN58833/c
 ID ACN58833 standard; cDNA; 514 BP.
 XX
 AC ACN58833;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Cotton gynoecium tissue EST Clone ID: LIB3829-012-Q6-N6-G10, SEQ:13614.
 XX
 KW Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium;
 variety Nuotton3B; library LIB3829; molecular tag; molecular marker;
 genetic mapping; molecular mapping; seed germination; plant growth;
 plant quality; plant yield; plant breeding; tissue printing; ss.
 XX
 OS Gossypium hirsutum.
 XX
 PN US2004123340-A1.
 XX
 PD 24-JUN-2004.
 XX
 PF 12-DEC-2001; 2001US-00021323.
 XX
 PR 14-DEC-2000; 2000US-0255619P.
 XX
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 XX
 PI Deikman J, Feng PCC, Fincher KL, Ziegler TE;
 WIPI; 2004-479808/45.

PT New isolated nucleic acid molecule that encodes a plant protein or its
 fragment, useful for isolating a variety of agronomically significant
 genes associated with plant growth, quality or yield, and as molecular
 tags to map genes.
 PS
 XS Claim 1; SEQ ID NO 13614; 34pp; English.
 XX
 CC The invention relates to 17880 cotton expressed sequence tags (ESTs;
 ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated
 from primed or non-primed seeds from variety DP50B, mature seeds from
 variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
 tissue, developing fibres, carpel walls and septa from variety
 Nuotton3B. The invention also relates to substantially purified
 proteins or their fragments encoded by nucleic acid molecules of the
 invention, and to transformed plants having a nucleic acid construct
 comprising a nucleic acid of the invention. The cotton ESTs are useful as
 molecular tags to isolate genetic regions, to isolate genes, to map
 genes, to determine gene function and to determine whether genes are
 members of a particular gene family. The nucleic acid molecules may be
 used for isolating a variety of agronomically significant genes
 associated with plant growth, quality, yield, and could also serve as

CC links in metabolic and catabolic pathways. The nucleic acid molecules are
 also useful for identifying genes important in initiating and maintaining
 seed germination or that may be used to mitigate stresses encountered
 during seed germination. The ESTs additionally enable the acquisition of
 promoters and cis-regulatory elements which will be useful to express
 agronomically significant genes in these tissues and/or other tissues,
 and also permits the acquisition of molecular markers useful in breeding
 schemes, genetic and molecular mapping, and in cloning of agronomically
 significant genes. The nucleic acid molecules are further useful for
 detecting the expression level or pattern of a protein or mRNA and for
 detecting the presence or quantity of a protein by tissue printing. The
 present sequence represents a specifically claimed EST isolated from a
 cotton variety Nuotton3B gynoecium tissue cDNA library (LIB3829). The
 sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the US
 patent office at seqdata.uspto.gov/sequence.html?DocID=US20040123340
 XX

Sequence 514 BP; 136 A; 124 C; 90 G; 164 T; 0 U; 0 Other;
 Query Match 9.3%; Score 158.6; DB 13; Length 514;
 Best Local Similarity 70.4%; Pred. No. 5e-34;
 Matches 212; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 1162 AGGGCCGTGGAGAAATGCTTTTGAAGATAACAATTGAAGCAATGGCATTCAAGTGGCCAG 1221
 |||||
 Db 514 AGGGACGGGGAGAAATGCTTTGGACGGATAACAATCGAAGCAATGGCATTTCAGTTGCCTG 455
 |||||
 QY 1222 TATTCGGCACGGCTCTGAGGGGACCGAGATGCTCTGACGGCTGACTGGCCTTC 1281
 |||||
 Db 454 TGCTGGGAACAGCTCCGGGGGCAACACGAAATAGTAGAACCGGCACACAGGTTTAT 395
 |||||
 QY 1282 TGCATCTCTGCTGGGAAGGAGGGCGTGGCGCTTTGCAAGAACATCGTCAGACTCGCAA 1341
 |||||
 Db 394 TGCACCTCTGCTGGGAAGAGAGGGGTGACAACTCTGGCGAACAATATTGTGAACACTAGCTA 335
 |||||
 QY 1342 GCCACGGCAGCAGAGGGTCTCCATGGGGGAAAGGGCTATGGCAGGGTGAAGAGGAATGT 1401
 |||||
 Db 334 CGCATGTAGAGAGAGGGCTTCAATAGGAAGAGAGGGGTACGAAAGGGTGAAAGAGAT 275
 |||||
 QY 1402 TCATGGAGCACCATGGCTGAGAGGATCGCGCGGCTGTTGAAGGATGCTCTGAGGAAT 1461
 |||||
 Db 274 TCTAGAACATCAGATGGCAGAGAGAAATGGTGAAGTACTTAAAGAAAGCGTTGAGGAAGT 215
 |||||
 QY 1462 C 1462
 Db 214 C 214

RESULT 12
 AAA31140
 ID AAA31140 standard; DNA; 284 BP.
 XX
 AC AAA31140;
 XX
 DT 05-JUL-2000 (first entry)
 XX
 DE Plant microsatellite marker #101.
 XX
 KW Plant microsatellite sequence; core repeat sequence; detection; probe;
 DNA polymorphism; genome mapping; physical mapping; fingerprinting;
 variety identification; genetic variability evaluation; primer; ss.
 XX
 OS Eucalyptus grandis.
 XX
 PN WO9967421-A1.
 XX
 PD 29-DEC-1999.
 XX
 PF 25-JUN-1999; 99WO-NZ000092.
 XX
 PR 25-JUN-1998; 98US-00105307.
 XX
 PA (GENE-) GENESIS RES & DEV CORP LTD.

PA (FLET-) FLETCHER CHALLENGE FOREST LTD.
XX
PI Havukkala IJ, Bloksberg LN, Glenn M;
XX
DR WPI; 2000-116958/10.
XX
PT New plant microsatellite markers and associated flanking species for the
PT detection of polymorphic genetic markers.
XX
XX
XX Claim 1; Page 106; 392pp; English.
XX
XX Sequences AAA31040-A32093 represent novel plant microsatellite sequences
CC and associated flanking species. The sequences comprise a central core
CC repeat sequence, especially selected from the sequences AAA32094-A32096
CC with left and right flanking sequences. The polynucleotide sequences can
CC be used in the detection of DNA polymorphisms, in genome mapping, in
CC physical mapping, in positional cloning of genes, in variety
CC identification and in evaluation of genetic variability within and
CC between plant tissues, populations, cultivars, species and species
CC groups. They may also be used to design hybridization probes for
CC oligonucleotide fingerprinting and library screening and to design
CC primers for microsatellite-primed PCR. Microsatellite markers are useful
CC to locate specific economically useful genes in plant genomes
XX
SQ Sequence 284 BP; 97 A; 48 C; 73 G; 66 T; 0 U; 0 Other;

Query Match 9.1%; Score 154.6; DB 3; Length 284;
Best Local Similarity 74.0%; Pred. No. 4.9e-33;
Matches 196; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 568 CTGCTCTGAAGATCATGTTCTTAAAGTCTTCCGAAAGATTTTGTGGTCCATGAAA 627
DB 20 CTAGTCTCAAGACAATGTTCTTAGTGTCTCCCAAAAATTTTGTGGTGCATTCAGAAA 79

QY 628 TCGTGGCGGATTAAGTTGAAATATGTCAAACATCTTCCTTTGTCTGGAGCCA 687
DB 80 TGAAGAGGCAATATTTTCAAACTGGAGTATGTCAGACCTACCTATGTGGCAGGGCAA 139

QY 688 TGATTGATTCATACACGGCTGAGTATTTGGAATAGCAGGATACGATCGCTGAAA 747
DB 140 TGATTGATTCATACACAGCTGAAATACCTGGAAGACCAAGAACTCAAGAACGCTCTGGGA 199

QY 748 TACAGATGCCACAACTTATGTTTCACTGGGGAAATAGTAAAGAACTAATGGAAGTTG 807
DB 200 TCAAGATGCTTAGACTTATGTCGACCTTGGAAATAGCCATGAAATTAATGGAAGTAG 259

QY 808 CTGAAGACAATGTCGCAAGAAGAT 832
DB 260 CAGAAGATAATGTGGCCAAAGGGT 284

RESULT 13
ADT18408
ID ADT18408 standard; cDNA; 1964 BP.
XX
XX ADT18408;
XX
XX 13-JAN-2005 (first entry)
XX
XX Plant cDNA, Seq ID 3734.
XX
XX Plant; ss; gene; transgenic; cold tolerance; growth rate;
KW drought tolerance; disease resistance; galactomanan production;
KW plant growth regulator; heat tolerance; herbicide tolerance;
KW lignin production; extreme osmotic condition tolerance;
KW pathogens resistance; pest resistance; yield improvement; seed oil yield;
KW seed protein yield.
XX
XX Viridiplantae.
OS
XX US2004216190-A1.
PN
XX 28-OCT-2004.
PD

XX
PF 18-DEC-2003; 2003US-00739930.
XX
PR 28-APR-2003; 2003US-00424599.
PR 28-APR-2003; 2003US-00425115.
XX
PA (KOVA/) KOVALIC D K.
XX
PI Kovalic DK;
XX
XX WPI; 2004-757369/74.
XX
XX New recombinant DNA constructs useful in the field of biochemistry and
PT genetics, and in particular for producing transgenic plants with improved
PT biological characteristics.
XX
XX Claim 1; SEQ ID NO 3734; 14pp; English.
XX
XX The invention relates a recombinant DNA construct comprising a
CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
CC Arabidopsis, wheat and rape but the specification does not indicate which
CC sequences is derived from which organism. Also included is a method of
CC producing a plant having an improved property, comprising transforming a
CC plant with a recombinant DNA construct comprising a promoter region
CC functional in a plant cell operably joined to a polynucleotide encoding a
CC polypeptide associated with the property, and growing the transformed
CC plant. The property is selected from improving plant cold tolerance, for
CC manipulating growth rate in plant cells by modification of the cell cycle
CC pathway, for improving plant drought tolerance, for providing increased
CC resistance to plant disease, for galactomanan production, for production
CC of plant growth regulators, for improving plant heat tolerance, for
CC improving plant tolerance to herbicides, for increasing the rate of
CC homologous recombination in plants, for lignin production, for improving
CC plant tolerance to extreme osmotic conditions, for improving plant
CC tolerance to pathogens or pests, for yield improvement by modification of
CC photosynthesis, for modifying seed oil yield and/or content, for
CC modifying seed protein yield and/or content, for yield improvement by
CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake
CC and for yield improvement by providing improved plant growth and
CC development under at least one stress condition. The polynucleotide may
CC also encode a plant transcription factor. The methods and compositions of
CC the present invention are useful in the field of biochemistry and
CC genetics, in particular for producing transgenic plants with improved
CC biological characteristics such as increased yield, improved nitrogen
CC flow, increasing plant tolerance to cold or heat, improving plant
CC tolerance to extreme osmotic and drought conditions, and improving plant
CC tolerance to plant pests or pathogens. They can also be used in physical
CC arrays of molecules, plant breeding markers, computer-based storage and
CC analysis systems. The present sequence is one of the 5544 plant cDNA
CC sequences of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20040216190.
XX
XX Sequence 1964 BP; 671 A; 323 C; 378 G; 592 T; 0 U; 0 Other;
SQ

Query Match 4.3%; Score 74; DB 13; Length 1964;
Best Local Similarity 67.5%; Pred. No. 1.1e-09;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1306 TGGCGCTCTTCAAGACATCGTCAGACTCGCAGCCACGCCGAGCAGAGGCTCTCCA 1365
DB 1373 TAGCCCTCTCGCGGAGAACATTTGAAATTTGCTAGTCTATTTGAGAGAGGCTTACAA 1432
QY 1366 TGGGGGAAAAGGCTATGCGAGGTCGAGGAAATGTTTCATGGAGCACCATGGCTGAGA 1425
DB 1433 TGGTAAGAAGAGATATGAGAGTGAAGGAAGGTTTGTGGCCACACATGTCACAGA 1492

QY 1426 GATCGCGCGGTGTTGAAGGATGTCTCTGAGGAA 1459
DB 1493 GAATCGAATTTGGTCTGGAAGGAAGTGTTCACAGAA 1526

PR	22-JUN-1998;	98US-0090170P.
PR	26-JUN-1998;	98US-0090928P.
PR	29-JUN-1998;	98US-0091035P.
PR	30-JUN-1998;	98US-0091405P.
PR	08-JUL-1998;	98US-0092036P.
PR	09-SEP-1998;	98US-0099667P.
PR	09-SEP-1998;	98US-0099670P.
PR	09-SEP-1998;	98US-0099697P.
PR	16-SEP-1998;	98US-0100672P.
PR	16-SEP-1998;	98US-0100673P.
PR	16-SEP-1998;	98US-0100674P.
PR	21-SEP-1998;	98US-0101130P.
PR	21-SEP-1998;	98US-0101131P.
PR	21-SEP-1998;	98US-0101132P.
PR	22-SEP-1998;	98US-0101134P.
PR	22-SEP-1998;	98US-0101344P.
PR	22-SEP-1998;	98US-0101347P.
PR	22-SEP-1998;	98US-0101508P.
PR	25-SEP-1998;	98US-0101707P.
PR	13-OCT-1998;	98US-0104123P.
PR	13-OCT-1998;	98US-0104124P.
PR	13-OCT-1998;	98US-0104126P.
PR	13-OCT-1998;	98US-0104127P.
PR	13-OCT-1998;	98US-0104128P.
PR	18-NOV-1998;	98US-0108998P.
PR	19-NOV-1998;	98US-0109018P.
PR	24-NOV-1998;	98US-0109112P.
PR	08-DEC-1998;	98US-00210297.
PR	11-DEC-1998;	98US-0111981P.
PR	22-DEC-1998;	98US-0113224P.
PR	12-JAN-1999;	99US-00229413.
XX		
	(CHEI/) CHEIKH N.	
	(FISH/) FISHER D K.	
	(LIU/) LIU J.	
PI	Cheikh N, Fisher DK, Liu J;	
XX	WPI; 2003-688722/65.	
DR		
XX		
PT	New maize or soybean enzymes and nucleic acid molecules associated with	
PT	the sucrose pathway, useful for genome mapping, gene identification and	
PT	analysis, plant breeding, or preparation of constructs for plant gene	
XX	expression.	
PS	Claim 2; Page; 117pp; English.	
XX		
CC	The invention relates to a substantially purified nucleic acid molecule	
CC	(appearing as ADA57847 - ADA60660 that encodes a maize or soybean enzyme	
CC	or its fragment, associated with the sucrose pathway selected from:	
CC	triase phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose	
CC	1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucoseisomerase,	
CC	vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent	
CC	fructose 6-phosphate phosphotransferase, invertase, sucrose synthase,	
CC	hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,	
CC	glucose-6-phosphate 1-dehydrogenase, phosphoglucomutase and uridine	
CC	diphosphate (UDP)-glucose pyrophosphorylase. Also included are a	
CC	substantially purified maize or soybean enzyme (or its fragment) and a	
CC	transformed plant having a nucleic acid molecule. Also disclosed as new	
CC	are purified antibodies capable of specifically binding to the maize or	
CC	soybean enzyme, determining a level or pattern of a plant sucrose pathway	
CC	enzyme in a plant cell or plant tissue, determining a mutation in a plant	
CC	whose presence is predictive of a mutation affecting the level or pattern	
CC	of a plant sucrose pathway enzyme, producing a plant containing an	
CC	overexpressed or reduced level of plant sucrose pathway enzyme, reducing	
CC	expression of a plant sucrose pathway enzyme in a plant and determining	
CC	an association between a polymorphism and a plant trait. The maize or	
CC	soybean enzymes and nucleic acid molecules are useful for genome mapping,	
CC	gene identification and analysis, plant breeding, or preparation of	
CC	constructs for plant gene expression and transgenic plants. The nucleic	
CC	acid molecules are also useful as markers or probes. The present sequence	
CC	is a soybean EST (expressed sequence tag) from a gene encoding a sucrose	
CC	pathway enzyme. Note: The sequence data for this patent did not form part	

CC of the printed specification, but was obtained in electronic format
 CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.

XX SQ Sequence 254 BP; 61 A; 53 C; 68 G; 69 T; 0 U; 3 Other;

Query Match 4.0%; Score 67.4; DB 9; Length 254;
 Best Local Similarity 60.5%; Pred. No. 2.5e-08;
 Matches 127; Conservative 0; Mismatches 82; Indels 1; Gaps 1;
 QY 1116 GTGGCCCTTACTTGGCAGCAATGATGCTGTGTTGTCAGAAATCTCAGGCGCGTGAGAA 1175
 Db 11 GTTGCTCACTTACTTCTGCCGAGATGTTATGTTATAAACTCTCAGGCGCGTGAGAA 70
 QY 1176 TCGTTGGNAGATACAAATGCAAGCAATGCAATTCAGTTCCAGTATTTGGGCGCGCT 1235
 Db 71 ACATTTGGACGTGTGACTATAGAACCAATGGCGTTTGGCTTCCGGTCTTTGGGACGGAC 130
 QY 1236 GTGGAGGACCAACGAGATGCTCTGGACGGCTCGACTGGGCTTCTGCATCTCTGGG 1295
 Db 131 GCTGGAGGACACAGAGATGTTGAGCAATGTTACAGGTC-TCTTCATCTCTGTTGA 189
 QY 1296 AAGGAGGCGTGGCGCTCTTGCAGAAAGAC 1325
 Db 190 CATCCGGGCAATCTTCTTTCANAGATC 219

RESULT 15
 ADQ06025
 ID ADQ06025 standard; DNA; 254 BP.
 AC ADQ06025;
 XX DT 09-SEP-2004 (first entry)
 XX DE Soybean transcription factor seqid 2871.
 XX KW maize; soybean; Arabidopsis thaliana; transcription factor; homeobox;
 KW HLH; leucine zipper; zinc finger; transformed plant; plant; trait;
 KW metabolic pathway; mutation detection; polymorphism; plant breeding;
 KW genome mapping; gene identification; gene analysis; plant breeding;
 KW transgenic; ds.
 XX OS Glycine max.
 XX PN US2004123339-A1.
 XX PD 24-JUN-2004.
 XX PF 06-AUG-2001; 2001US-00922293.
 XX PR 24-NOV-1997; 97US-0067000P.
 PR 09-DEC-1997; 97US-0069472P.
 PR 13-JAN-1998; 98US-0071479P.
 PR 10-FEB-1998; 98US-0074201P.
 PR 10-FEB-1998; 98US-0074280P.
 PR 10-FEB-1998; 98US-0074281P.
 PR 10-FEB-1998; 98US-0074282P.
 PR 12-FEB-1998; 98US-0074565P.
 PR 12-FEB-1998; 98US-0074566P.
 PR 12-FEB-1998; 98US-0074567P.
 PR 19-FEB-1998; 98US-0074789P.
 PR 19-FEB-1998; 98US-0075459P.
 PR 19-FEB-1998; 98US-0075460P.
 PR 19-FEB-1998; 98US-0075461P.
 PR 19-FEB-1998; 98US-0075462P.
 PR 19-FEB-1998; 98US-0075463P.
 PR 19-FEB-1998; 98US-0075464P.
 PR 09-MAR-1998; 98US-0077229P.
 PR 09-MAR-1998; 98US-0077230P.
 PR 18-MAR-1998; 98US-0077231P.
 PR 07-APR-1998; 98US-0078368P.
 PR 27-APR-1998; 98US-0080844P.
 PR 98US-0083067P.

PR 29-APR-1998; 98US-0083386P.
 PR 29-APR-1998; 98US-0083387P.
 PR 29-APR-1998; 98US-0083388P.
 PR 29-APR-1998; 98US-0083389P.
 PR 13-MAY-1998; 98US-0085222P.
 PR 13-MAY-1998; 98US-0085223P.
 PR 13-MAY-1998; 98US-0085224P.
 PR 15-MAY-1998; 98US-0085533P.
 PR 21-MAY-1998; 98US-0086183P.
 PR 21-MAY-1998; 98US-0086184P.
 PR 21-MAY-1998; 98US-0086185P.
 PR 21-MAY-1998; 98US-0086186P.
 PR 21-MAY-1998; 98US-0086187P.
 PR 21-MAY-1998; 98US-0086188P.
 PR 16-JUN-1998; 98US-0085524P.
 PR 18-JUN-1998; 98US-0089793P.
 PR 18-JUN-1998; 98US-0089806P.
 PR 18-JUN-1998; 98US-0089807P.
 PR 18-JUN-1998; 98US-0089808P.
 PR 18-JUN-1998; 98US-0089810P.
 PR 18-JUN-1998; 98US-0089811P.
 PR 18-JUN-1998; 98US-0089812P.
 PR 18-JUN-1998; 98US-0089813P.
 PR 18-JUN-1998; 98US-0089814P.
 PR 30-JUN-1998; 98US-0091247P.
 PR 30-JUN-1998; 98US-0091405P.
 PR 09-SEP-1998; 98US-0099667P.
 PR 09-SEP-1998; 98US-0099668P.
 PR 09-SEP-1998; 98US-0099670P.
 PR 09-SEP-1998; 98US-0099677P.
 PR 16-SEP-1998; 98US-0100672P.
 PR 16-SEP-1998; 98US-0100673P.
 PR 16-SEP-1998; 98US-0100674P.
 PR 17-SEP-1998; 98US-0100963P.
 PR 21-SEP-1998; 98US-0101130P.
 PR 21-SEP-1998; 98US-0101131P.
 PR 21-SEP-1998; 98US-0101132P.
 PR 22-SEP-1998; 98US-0101343P.
 PR 22-SEP-1998; 98US-0101344P.
 PR 22-SEP-1998; 98US-0101347P.
 PR 22-SEP-1998; 98US-0101508P.
 PR 25-SEP-1998; 98US-0101707P.
 PR 13-OCT-1998; 98US-0104124P.
 PR 13-OCT-1998; 98US-0104126P.
 PR 13-OCT-1998; 98US-0104127P.
 PR 13-OCT-1998; 98US-0104128P.
 PR 18-NOV-1998; 98US-0108996P.
 PR 19-NOV-1998; 98US-0109018P.
 PR 24-NOV-1998; 98US-00199129.
 PR 08-DEC-1998; 98US-00210297.
 PR 11-DEC-1998; 98US-0111981P.
 PR 22-DEC-1998; 98US-0113224P.
 PR 12-JAN-1999; 99US-00229413.

(CONN/) CONNER T W.
 (HECK/) HECK G R.
 (LIU/) LIU J.

Conner TW, Heck GR, Liu J;
 WPI; 2004-468202/44.

New substantially purified nucleic acid molecule that encodes a maize,
 PT soybean or Arabidopsis thaliana transcription factor or its fragment,
 PT useful for genome mapping, gene identification and analysis or plant
 PT breeding.

PS Claim 2; SEQ ID NO 2871; 140pp; English.

XX The invention describes a substantially purified nucleic acid molecule
 CC that encodes a maize, soybean or Arabidopsis thaliana transcription
 CC factor or its fragment, where the maize or soybean transcription factor
 CC is homeobox, HLH, leucine zipper, zinc finger, or other transcription

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OM nucleic - nucleic search, using sw model

Run on: March 17, 2006, 02:40:52 ; Search time 323 Seconds
(without alignments)
9366.594 Million cell updates/sec

Title: US-09-938-294-2

Perfect score: 1702

Sequence: 1 attcgctcgattgatcc.....gaggagattcaatcttagt 1702

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

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5: /cgn2_6/prodata/1/ina/H COMB.seq.*
6: /cgn2_6/prodata/1/ina/ECTUS COMB.seq.*
7: /cgn2_6/prodata/1/ina/PP COMB.seq.*
8: /cgn2_6/prodata/1/ina/RE COMB.seq.*
9: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	2.9	832	3	US-09-621-976-2813
2	49.2	2.9	1926	3	US-09-249-585A-4
3	49.2	2.9	1931	2	US-09-130-114-2
4	49	2.9	5877	3	US-10-152-886-54
5	48.4	2.8	1082	3	US-09-881-165-4
6	48.2	2.8	912	3	US-09-347-504-11
7	48.2	2.8	912	3	US-08-902-572-13
8	48.2	2.8	912	3	US-10-161-499-11
9	48.2	2.8	950	3	US-09-230-421-1
10	48.2	2.8	6404	3	US-09-937-837-1
11	48.2	2.8	6420	3	US-09-937-837-2
12	47.4	2.8	7218	2	US-08-232-463-14
13	46.8	2.7	43280	2	US-08-804-227C-1
14	46.6	2.7	954	3	US-08-680-506-5
15	46.6	2.7	1239	3	US-09-902-540-7944
16	46.6	2.7	1347	3	US-08-680-506-8
17	46.6	2.7	1587	3	US-08-680-506-6
18	46.6	2.7	2233	3	US-08-680-506-4
19	46.6	2.7	5027	3	US-08-680-506-2
20	46.6	2.7	11922	3	US-09-902-540-1063
21	46.4	2.7	21721	3	US-09-269-939A-41
22	46.4	2.7	23187	3	US-09-499-522-1
23	46.2	2.7	4403765	3	US-09-103-840A-2
24	46.2	2.7	4411529	3	US-09-103-840A-1

25	46	2.7	1905	3	US-09-142-623-2	Sequence 2, Appli
26	45.8	2.7	18551	3	US-09-902-540-1187	Sequence 1187, Ap
27	45.6	2.7	40586	3	US-09-949-016-16965	Sequence 16965, A
28	45.6	2.7	670689	3	US-09-949-016-12505	Sequence 12505, A
29	45.6	2.7	670690	3	US-09-949-016-14207	Sequence 14207, A
30	44.6	2.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
31	44.6	2.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
32	44.4	2.6	1578	3	US-09-252-991A-13064	Sequence 13064, A
33	44.4	2.6	1824	3	US-09-252-991A-12570	Sequence 12570, A
34	44.4	2.6	44377	2	US-08-804-227C-7	Sequence 7, Appli
35	44.4	2.6	44377	2	US-08-804-198-1	Sequence 1, Appli
36	44.2	2.6	1281	3	US-09-252-991A-12717	Sequence 12717, A
37	44.2	2.6	2855	3	US-09-904-420A-1	Sequence 1, Appli
38	44	2.6	47181	3	US-09-949-016-16131	Sequence 16131, A
39	44	2.6	47181	3	US-09-949-016-16132	Sequence 16132, A
40	44	2.6	47181	3	US-09-949-016-16133	Sequence 16133, A
41	43.8	2.6	1141	3	US-09-806-708B-22	Sequence 22, Appli
42	43.8	2.6	1434	3	US-09-902-540-4356	Sequence 4356, Ap
43	43.8	2.6	1822	3	US-09-949-016-1464	Sequence 1464, Ap
44	43.8	2.6	1965	3	US-09-220-132-21	Sequence 21, Appli
45	43.8	2.6	9399	3	US-09-949-016-13206	Sequence 13206, A

ALIGNMENTS

RESULT 1
US-09-621-976-2813
; Sequence 2813, Application US/09621976
; Patent No. 6639083
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

Query Match		2.9%	Score 50;	DB 3;	Length 832;
Best Local Similarity		11.1%	Pred. No. 0.0016;		
Matches 39;		Conservative 183;	Mismatches 128;	Indels 2;	Gaps 2;
QY	876	GATCTCTGTTGCAATTAATAACAGTGTATCACGAGGAAGGACAGACTATTTCCT	935		
DB	2	RYWKKYTTAKCWTWKWMSYWKYWKYTKYTWKWKYWKYTKYTWKWKY	61		
QY	936	CAAGCATTTTATCAGGCTTTGCAG-CTCATCAACACGAGAACTTAAAGTCCTAGAT	994		
DB	62	YAMWGTYYKKKAWCRRTTKKKKKGGYMMWYWGWRSSYMAWTRTWTGYAYRSMYWKY	121		
QY	995	ACATGCTGTAGTGTGGGAAGTGATGTTAATGCTCAGACCAATTTGAGACTCAGTTAGC	1054		
DB	122	RCWKKKAYYRKTTCYSSKGWTKWKKKAWTTTWWKKTYWATRYMMWCMWKWRASW	181		
QY	1055	TGACTTTGTTGGAAGACACGATTCATGACCGTGTCCATTTTGTGACACAGACTTGC	1114		
DB	182	WYCWGKARKWSTWRKRSYASARSARECCYSCSWGAMSWKYMWRMWRGM-ATGAG	240		
QY	1115	AGTGCCCTTACTTGGGAGCAATTTGATGTGTTGTCAGATTCTCAGGGCGGTGAGA	1174		
DB	241	KAWRASCMRRKRYAGSKTSYKSMCMWTRSWKYCTTKARWTGYCYRKGWGRGRWY	300		

Qy	3	TCGGTTCGAGTTTGATCGAGGCCACAGTCTCTCTCGGGCCCAACGGGTCCGACCGGGC	62
Db	325	TCCGAGGGCGGACGACACCCACACCGCCCCCGGGCCCCCGAACCACGCGGGTG	384
Qy	63	ATGCAAGAGACCCCGTCGTCGGTGGGGCGGTTCGCCGAGGCGCGGGCCGGTTTCAC	122
Db	385	GCGACTAAGGCCCCCGCGGCCCGCGCGGAGACACCCCGGCAGGAAATCGGCCACG	444
Qy	123	AACGGACCCAGCTCTCTCTCTCTCGTGGCGCTCGCAGCCTTCGCGATCCACAGCA	182
Db	445	CCAGATCCGGCGGCACTCCAGACGCCCCCGCGTCGACGGCGCAACCGATCCAGACA	504
Qy	183	GGGTTCTCTCTCGCGGTGCCCTGTGCGAGACCTTTCGAGCGCCGTGGGACCCCGCGCC	242
Db	505	CCCGCGCAGGGGCTGGCCAGAAAGTGCACCTTAGCACCGCCCCCCCCAAACCCCGACGG	564
Qy	243	CTCAACACCGCGTCGCGAGGGGAGTCCCCTCGGGTTCAATGAGTTCGAAGCTCGTGTC	302
Db	565	CCATGGACCCCCCGGTGGCGGGCTTAACAAGCGCTCTTCTGGCGCGCGTCTGGGGCC	624
Qy	303	CTCGTCTCC	311
Db	625	CTGGCGGCC	633

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RESULT 8
US-10-161-499-11
; Sequence 11, Application US/10161499
; Patent No. 6673354
; GENERAL INFORMATION:
; APPLICANT: Howley, Peter M.
; APPLICANT: Benson, John
; APPLICANT: Kasukawa, Hiroaki
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS
; FILE REFERENCE: HMV-041.01
; CURRENT APPLICATION NUMBER: US/10/161,499
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/347,504
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 912
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Ndel-EcoRI
; OTHER INFORMATION: fragment
US-10-161-499-11

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	Query Match	2.8%;	Score 48.2;	DB 3;	Length 912;
	Best Local Similarity	47.2%;	Pred. NO. 0.0054;		
	Matches 146;	Conservative 0;	Mismatches 163;	Indels 0;	Gaps 0;
Qy	3	TGGGCTCAGTTTGATCCGAGGCCACAGTCTCTCGGGGCCACCGCGTCGGAACCGGCG	62		
Db	325	TCCGAGGGGCGGACGCACACCACACCGCCCCCGGGCCCCCGAACCAGCGGGGTG	384		
Qy	63	ATGGCAAAAGACCCCCTGTTGCGCGTGGCGGCGGTGCGCGGAGGCGCGGGCGCGGTTTCAC	122		
Db	385	CGACTAAGGCCCCCGCGCCCCGCGGGGAGACCAACCCGGGCGAGGAATCGGCCACG	444		
Qy	123	AACGGGACCCAGTCTCTCTCTCTCTCTGTFGGCCGTGCGAGCTCTCGCATTCACAGA	182		
Db	445	CCAGAACTCCGGCGCACTCCACAGACCCCCCGCGTCCGACGGGGCCAACCCGATCCAAAGACA	504		
Qy	183	GGGTTCTCTCTCGGCGGTGCCCTGCGAGACCTTTCGACGCGCGTGGGGACCCCGCGCGC	242		
Db	505	CCCGGCGCAGGGGCTGGCCAGAAAGCTGTGCACTTTTAGCACCGCCCCCCCCCAAACCCCGACGCG	564		
Qy	243	CTCAACACCGCGCGTGC CGCAGCGGGAGTCCCCTCTCGGGTTTCATGAGGTCCAAGCTCGTGTC	302		

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Db      565  CCATGGACCCCGCGGTGGCGGCTTTAA CAAAGCGCGTCTTCTGCGCCGCGGTGCGGCGC 624
Qy      303  CTCGTCCTCC 311
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          |||
Db      625  CTGGCGGCC 633

RESULT 9
US-09-230-421-1
; Sequence 1, Application US/092330421
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 950
; TYPE: DNA
; ORGANISM: HERPESVIRUS TYPE 1
US-09-230-421-1

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	Query Match	2.8%;	Score 48.2;	DB 3;	Length 950;
	Best Local Similarity	47.2%;	Pred. No. 0.0055;		
	Matches 146;	Conservative 0;	Mismatches 163;	Indels 0;	Gaps 0;
Qy	3	TCGGCTCGAGTTTCATCCGAGCCACACAGTCTCTCTCGGGGCCACCGGTCCGACCGGGC	62		
Db	366	TCGGAGGGGCGGACGACACCCACACACCCGCCCGGGGCCCCCGAACCCAGCGGGTG	425		
Qy	63	ATGCCAAAGACCCCGTCTTCGCGGTGGCGCGGTTCGCCGAGGCCGGGGCCGGTTTCAC	122		
Db	426	GCGACTAAGGCCCCCGCGGCCCGCGGGCGAGACCACTCCGCGGCAGGAAATCGGCCAC	485		
Qy	123	AACCGGACACAGTCTCTCTCTCTCTCTGTGGCGGTTCGAGACCTTCGCGATCCACAGCA	182		
Db	486	CCAGATCCGCGGCACATCCACAGACGCCGCCCGCGTTCGACGGGGCCAAACCCGATCCAGACA	545		
Qy	183	GGGTTCCTCTCCGCGGTGCCCTTCGAGACCTTCGACAGCGCGTGGGGACCCCGCCGCC	242		
Db	546	CCCGCGCAGGGGCTGGCCAGAAAGTGCACCTTTAGCACCGCCCCCCCCAACCCCGACCGC	605		
Qy	243	CTCAACACCCGCGTCGCGCAGCGGGAGTCCCTCTCGGGTTTCATGAGTTCCAAGCTCTGGTCTC	302		
Db	606	CCATGGACCCCGGGTGGCGGCTTTTAAACAGCGCTCTTCGTGCGCGCGGTTCGGGCGC	665		
Qy	303	CTCGTCTCC	311		
Db	666	CTGGCGGC	674		

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RESULT 10
US-09-937-837-1
; Sequence 1, Application US/09937837
; Patent No. 6773920
; GENERAL INFORMATION:
; APPLICANT: INVITROGEN CORPORATION
; APPLICANT: DALBY, Brian
; APPLICANT: BENNETT, Robert
; TITLE OF INVENTION: DELIVERY OF FUNCTIONAL PROTEIN SEQUENCES
; TITLE OF INVENTION: BY TRANSLOCATING POLYPEPTIDES
; FILE REFERENCE: INVIT1280-1
; CURRENT APPLICATION NUMBER: US/09/937,837
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: PCT/US00/08571
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/127,467
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ IDS NOS: 21

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SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 6404
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: vector pVP22/Myc-His
 US-09-937-837-1

Query Match 2.8%; Score 48.2; DB 3; Length 6404;
 Best Local Similarity 47.2%; Pred. No. 0.015;
 Matches 146; Conservative 0; Mismatches 163; Indels 0; Gaps 0;
 QY 3 TCGGCTCGAGTTTGTATCCGAGCCACAGTCTCTCTCGGGGCCACCGCGTCCGACCGGG 62
 DB 1232 TCGGAGGGGCGGAGGACACCCACCGCCCGGGGGGGGGGGGGGGGGGGGGGGGGGG 1291
 QY 63 ATGGCAAGACCCGCTGCTTCCGGTGGGGGGGGTGGCGAGGCGGGGGGGGGTTCAC 122
 DB 1292 GCGTCTAAGGGCCCGCGGGCCCGGGCGGAGACACCCCGGGGAGAAATCGGGCCAG 1351
 QY 123 AACCGACCCAGCT 182
 DB 1352 CCAGATCCGCGCACTCCAGACGCGCCCGCGGTGACATTTAGACCGCCCAACCGATCCAAGACA 1411
 QY 183 GGGTCT 242
 DB 1412 CCCGCGAGGGGCTGCGCAGAAAGTGCATTTAGACCGCCCAACCGCCCAACCGCGG 1471
 QY 243 CTCACACCGCGCTGCCAGCGGAGTCCCTCTCGGGTTTCATGAGTTCAGGTTCGTGTC 302
 DB 1472 CCATGGACCCCGGGTGGCGGCTTTAAAGAGCGGCTTTCTGCGCGCGGTGCGGGCG 1531
 QY 303 CTCGCTCTCC 311
 DB 1532 CTGGCGGCC 1540

RESULT 11
 US-09-937-837-2
 Sequence 2, Application US/09937837
 Patent No. 6773920
 GENERAL INFORMATION:
 APPLICANT: INVITROGEN CORPORATION
 APPLICANT: DALBY, Brian
 APPLICANT: BENNETT, Robert
 TITLE OF INVENTION: DELIVERY OF FUNCTIONAL PROTEIN SEQUENCES
 FILE REFERENCE: INVIT1280-1
 CURRENT FILING DATE: 2001-09-28
 PRIOR FILING DATE: 2000-03-31
 PRIOR FILING DATE: 2000-03-31
 PRIOR FILING DATE: 1999-03-31
 NUMBER OF SEQ ID NOS: 21
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 6420
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: vector pVP22/Myc-His-TOPO
 US-09-937-837-2

Query Match 2.8%; Score 48.2; DB 3; Length 6420;
 Best Local Similarity 47.2%; Pred. No. 0.015;
 Matches 146; Conservative 0; Mismatches 163; Indels 0; Gaps 0;
 QY 3 TCGGCTCGAGTTTGTATCCGAGCCACAGTCTCTCTCGGGGCCACCGCGTCCGACCGGG 62
 DB 1232 TCGGAGGGGCGGAGGACACCCACCGCCCGGGGGGGGGGGGGGGGGGGGGGGGGGG 1291

QY 63 ATGGCAAGACCCCGTCT 122
 DB 1292 GCGACTAAGGGCCCGCGGGCCCGGGCGGAGACACCCCGGGGAGAAATCGGGCCAG 1351
 QY 123 AACCGACCCAGCT 182
 DB 1352 CCAGATCCGCGCACTCCAGACGCGCCCGCGGTGACATTTAGACCGCCCAACCGATCCAAGACA 1411
 QY 183 GGGTCT 242
 DB 1412 CCCGCGAGGGGCTGCGCAGAAAGTGCATTTAGACCGCCCAACCGCCCAACCGCGG 1471
 QY 243 CTCACACCGCGCTGCCAGCGGAGTCCCTCTCGGGTTTCATGAGTTCAGGTTCGTGTC 302
 DB 1472 CCATGGACCCCGGGTGGCGGCTTTAAAGAGCGGCTTTCTGCGCGCGGTGCGGGCG 1531
 QY 303 CTCGCTCTCC 311
 DB 1532 CTGGCGGCC 1540

RESULT 12
 US-08-232-463-14
 Sequence 14, Application US/08232463
 Patent No. 5670367
 GENERAL INFORMATION:
 APPLICANT: DORNER, F.
 APPLICANT: SCHEIFLINGER, F.
 APPLICANT: FALKNER, F. G.
 TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 1800 Diagonal Road, Suite 500
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22313-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,463
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/935,313
 FILING DATE:
 APPLICATION NUMBER: EP 91 114 300.6
 FILING DATE: 26-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 30472/114 IMMU
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)836-9300
 TELEFAX: (703)683-4109
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7218 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 CLONE: pTZgpt-F1s
 US-08-232-463-14

Query Match 2.8%; Score 47.4; DB 2; Length 7218;
 Best Local Similarity 4.4%; Pred. No. 0.026;
 Matches 12; Conservative 160; Mismatches 101; Indels 0; Gaps 0;

US-09-902-540-7944
; Sequence 7944, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 7944
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-7944

Query Match 2.7%; Score 46.6; DB 3; Length 1239;
Best Local Similarity 51.3%; Pred. No. 0.018;
Matches 137; Conservative 0; Mismatches 124; Indels 6; Gaps 1;

QY	1179	TTTGGAAAGGATAACAATTGAAGCAATGGCATTCAAGTTGCCAGTATTGGGCAACGGCTGCT	1238
Db	964	TTGGGGGTGGCCATCATGAGGCCATGGCCATGCGCGTCCCGTGGTGGTGACGGCGCG	1023
QY	1239	GGAGGACACCGAGATCTCTGGACGGCTCGACTGGCCCTTCTGCAATCTTCTGGGAAG	1298
Db	1024	GGTGGGGTCCCGAGTTGGTGATGACGGGGTGGACGGAATCTCGTCCCCCGCAGCAG	1083
QY	1299	GAGGGGTGGCGCTCTTGCAGAACATCGTCAGACTCGCAAGCCACGCCGAGCAGAGG	1358
Db	1084	CCCCGC-----ACCTGGCGGACAAAGCTGGAGACCGTGGCGCGCACGCCAGGAGGCC	1137
QY	1359	GTCTCCATGGGGGAAAAGGGCTATGGCAGGGTCAAGGAAATGTTATGGAGCACCACATG	1418
Db	1138	CACCGGCTGGTGAGCGGGCGCCGCAAGGTGGAGACGACGCTTCAGCAGCGGCGCAGC	1197
QY	1419	GCTGAGAGGATCGCGCGGTGTTGAAG	1445
Db	1198	GCGGACATGCTCGCGCAGATGCTCCAG	1224

Search completed: March 17, 2006, 04:44:36
Job time : 334 secs

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Result No.	Query			DB	ID	Description	
	Score	Match	Length				
1	1647	96.8	1647	7	US-10-425-114-3707	Sequence 3707, Ap	
2	1591.8	93.5	1853	8	US-10-425-115-103279	Sequence 103279, A	
3	10421.6	61.3	1449	7	US-10-437-963-39774	Sequence 39774, A	
4	776.4	45.6	1048	7	US-10-767-701-12116	Sequence 12116, A	
5	614.2	36.1	667	7	US-10-767-701-9892	Sequence 9892, Ap	
6	441.8	26.0	2395	7	US-10-424-599-64438	Sequence 64438, A	
7	426.2	25.0	1094	8	US-10-767-795-6175	Sequence 6175, Ap	
8	262	15.4	276	3	US-09-923-876-6035	Sequence 6035, Ap	
9	262	15.4	276	3	US-09-923-876-6035	Sequence 6035, Ap	
10	257	15.1	257	3	US-09-923-876-6078	Sequence 6078, Ap	
11	257	15.1	257	3	US-09-923-876-6078	Sequence 6078, Ap	
12	244.8	14.4	948	8	US-10-767-795-3626	Sequence 3626, Ap	
c	13	233	583	3	US-09-770-152-133	Sequence 133, App	
	14	227	13.3	625	7	US-10-021-323-13572	Sequence 13572, A
	15	227	13.3	625	8	US-10-767-795-3627	Sequence 3627, Ap
16	217.2	12.8	909	7	US-10-424-599-77966	Sequence 77966, A	
17	210	12.3	382	8	US-10-767-795-6176	Sequence 6176, Ap	
18	196.6	11.6	345	8	US-10-425-115-163392	Sequence 163392, A	
19	179.6	10.6	537	7	US-10-424-599-53829	Sequence 53829, A	
c	20	158.6	9.3	514	7	US-10-021-323-13614	Sequence 13614, A
21	154.6	9.1	284	5	US-10-062-727-101	Sequence 101, App	
c	22	148.6	8.7	396	8	US-10-425-115-173887	Sequence 173887, A
	23	144.4	8.5	665	7	US-10-424-599-53164	Sequence 53164, A


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Db 361 ATAAACACAGAGATCGGAGGAAACAAATGATGTACATATAGCTTGGAGCATAGATG 420
QY 456 TTGAACCATGGAGTCAGGTTTACAGCTAGAGGACAGGAGCGAGTTGATATGCTCTA 515
Db 421 TTGAGCCATGGAGTCAGGTTTACCTGCTAGGGGACATGAGCGGATGATATGCGCTTA 480
QY 516 AAAGCTGATCTGGTTATCTTAAACACTGCTGTTGCTGGCAAGTGGCTTACCCCTGTTCTG 575
Db 481 AAGGCTGATCTTGTATCTTGAACACTGCTGTTGCTGGCAAGTGGCTTATGCTGCTCTA 540
QY 576 AAAGATCATGTTCTTAAAGTCTCTTCCAAAGATTTTGTGGTGATCCATGAATGCGTGG 635
Db 541 AATGACCATGTTCCCAAGTCTTCCCAAGATTTTGTGGTGATCCATGAATGCGAGG 600
QY 636 CATTACTTAAAGTTGAATATATGCAAAACATCTTCCCTTTGTTGCTGGAGCCATGATGAT 695
Db 601 CATTACTTAAAGTTGAATATATGCAAAACATCTTCCCTTCTGTTGCTGGAGCCATGATGAT 660
QY 696 TCTCATACACGCTGAGTATTTGGATAGCAGGACTAGCGATCGCTGAAATACAGATG 755
Db 661 TCTCATACACGCTGAGTATTTGGATAGCAGGACTAGCGATCGCTGAAATACAGATG 720
QY 756 CCACAACTTATGTTGTTCACTCGGGAATAGTAAAGAACTAATGGAAGTGTCTGAAGAC 815
Db 721 CCACAACTTATGTTGTTCACTCGGGAATAGTAAAGAACTAATGGAAGTGTCTGAAGAT 780
QY 816 AATGTCGAAGAGTCTCTACGGGAACATATTCGTGAATCCCTTGGAGTAGCGAGTAG 875
Db 781 AATGTTGCAAGAGTCTCTACGGGAGCATATCCGTGAGTTCCTTGGAGTAGCGAGTAG 840
QY 876 GATCTCTGTTGCAATATTAACAGTGTATACGAGGAAAGGGAACAGTATTTCTT 935
Db 841 GATCTCTGTTGCAATATTAACAGTGTATACGAGGAAAGGGAACAGTATTTCTT 900
QY 936 CAAGCAATTTTATCAGGCTTTGAGCTTCATCCAAACAGAGAACTTAAAGTGTCTAGAA 995
Db 901 CAAGCGTTTATCAGGGTGTCCAGCTCATCGAACAGAGAGTAAAGTGTCCCAATG 960
QY 996 CATGCTGATGTTGGGAAGTGAATGTTAATGCTCAGACCAAAATTTGAGACTCAGTTACGT 1055
Db 961 CATGCTGATGTTGGGAAGTGAATGTTAATGCTCAGACCAAAATTTGAGACTCAGTTACGT 1020
QY 1056 GACTTTGCTGGAGAACAGTTCATGACCGTCCATTTTGTGAAACAGACATTTGGCA 1115
Db 1021 GATTTTGGGTAAGAAATGGGATTCAGGACCGGTTTCACTTTGTAAACAGACATTTAGCA 1080
QY 1116 GTGGCCCTTTACTTGGCAGCAATTTGATGTGCTTGTTCAGAAATCTCAGGGCCGTGAGAA 1175
Db 1081 GTGGCTCTTTATTTGGCTGCACTGATGTGCTTGTTCAGAACTCTCAGGCCCGTGGAA 1140
QY 1176 TGCTTTGGAAGGATTAACAATTTGAAGCAATGGCAATTTCAAGTTGCGCAGTATTTGGGACAGGCT 1235
Db 1141 TGCTTTGGAAGGATTAACAATTTGAAGCAATGGCAATTTCAAGTTGCGCAGTATTTGGGACAGGCT 1200
QY 1236 GCTGGAGGACACAGGATGCTTGGAGCGGCTCGACTGCGCTTCTGCTATCTGCTGCTGG 1295
Db 1201 GCGGAGGACACAGGATGCTTGGAGCGGCTCGACTGCGGCTTCTGCTATCTGCTGCTGG 1260
QY 1296 AAGGAGGCGGTGCGGCTCTTTCAGAAAGAAATCATGCTCAGACTTCGCAAGCCACGCGAGCAG 1355
Db 1261 AAGGAGGCGGTGCGGCTCTTTCAGAAAGAAATCATGTAAGGCTTCGCGAGCCACGAGAGGAC 1320
QY 1356 AGGGTCTCCATGCGGGGAAAGAGGCTATGCGAGGCTGAAGAAATGTTCTGAGAGCACAC 1415
Db 1321 AGGGTCTCCATGCGGGTGAAGAGGCTATGCGAGGCTGAAGAAATGTTCTGAGAGCACAC 1380
QY 1416 ATGGCTGAGAGGATCGCGGCTGTTGAGAGTGTCTGAGGAAATCAGAGGAGCACTCC 1475
Db 1381 ATGGCTGAGAGGATCGCGGCTGTTGAGAGTGTCTGAGGAAATCAGAGGAGCACTCC 1440
QY 1476 AGGTCTTTGA 1484

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Db 1441 CACTCTTGA 1449

RESULT 4
US-10-767-701-12116
; Sequence 12116, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 12116
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS10968_1
US-10-767-701-12116

Query Match 45.6%; Score 776.4; DB 7; Length 1048;
Best Local Similarity 95.7%; Pred. No. 4.4e-228;
Matches 798; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 655 ATGTCAAACATCTTCCCTTTGTTGCTGGAGCCATGATTCTCTATACACGGCTGAGT 714
Db 1 ATGTCAAACATCTTCCCTTTGTTGCTGGAGCCATGATTCTCTATACACGGCTGAA 60
QY 715 ATTGAATAGAGGACTAGCGATCGCTGAAAATACAGATGCCAACAATTATTTGTTTC 774
Db 61 ATTGAAGAGCAGGACTAGCGACCGCTTAAATAACAGATGCCAACAATTATTTGTTTC 120
QY 775 ACTCGGGAATAGTAAAGAACTTAAAGTGTCTGAAACAATGTGCGAAAGAGTCC 834
Db 121 ACTCGGGAATAGTAAAGAACTTAAAGTGTCTGAAACAATGTGCGAAAGAGTCC 180
QY 835 TACGGGAACATATTCGTGAATCCCTTGGAGTAGCGAGTGAGGATCTCTGTTTGCATAA 894
Db 181 TACGGGAACATATTCGTGAATCCCTTGGAGTAGCGAGTGAGGATCTCTGTTTGCATAA 240
QY 895 TAAACAGTGTATCAGGAAAGGACAGACTTATTTCTTCAAGCAATTTATCAGGCTT 954
Db 241 TAAACAGTGTATCAGGAAAGGACAGACTTATTTCTTCAAGCAATTTATCAGGCTT 300
QY 955 TGCAGCTCATCCAAACAGAGAACTTAAAGTGTCTAGAAATACATGCTGTAGTTTGGGAA 1014
Db 301 TGCAGCTCATCCAAACAGAGAACTTAAAGTGTCTAGAAATACATGCTGTAGTTTGGGAA 360
QY 1015 GTGATGTTAATGCTCAGACCAAAATTTGAGACTCAGTTACGTGATTTGTTGGTGAAGACA 1074
Db 361 GTGATGTTAATGCTCAGACCAAAATTTGAGACTCAGTTACGTGATTTGTTGGTGAAGATG 420
QY 1075 CGATTTCAGCGTGTCCATTTTGTGAAACAGACATTTGCGAGTGGCCCTTACTTGGCAG 1134
Db 421 CGATTTCAGCGTGTCCATTTTGTGAAACAGACATTTGCGAGTGGCCCTTACTTGGCAG 480
QY 1135 CAATTGATGCTGTTTTCAGAAATTTCTCAGGCGGCTGGAGAAATGCTTTTGAAGGATTAACA 1194
Db 481 CAATTGATGCTGTTTTCAGAAATTTCTCAGGCGGCTGGAGAAATGCTTTTGAAGGATTAACA 540
QY 1195 TTGAAGCAATGGCAATTTCAAGTTTCCAGTATTTGGGACGCGCTGCTGAGGAGCAACGAG 1254
Db 541 TTGAAGCAATGGCAATTTCAAGTTTCCAGTATTTGGGACGCGCTGCTGAGGAGCAACGAG 600
QY 1255 TGTCTCTGAGCGCTCGACTGCGCTTCTGATCTCTGCGAGGAGGCGGTGCGGCTC 1314
Db 601 TGTCTCTGAGCGCTCGACTGCGCTTCTGATCTCTGCGAGGAGGCGGTGCGGCTC 660

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QY 1012 GAATGATGTTAATGCTCAGACCAAAATTTGAGACTCAGTTACGTGACTTTTGTGCTGAAGA 1071
 DB 1255 GGAGTGATATGAATGCTCAGACAAAGTTTGAATGGAATCTTCGCAAAATTTGTGTGAGA 1314
 QY 1072 ACACGATTATGACCGGTGCTCAATTTTGTGAACAAGACATTTGGCAGTGGCCCTTACTTGG 1131
 DB 1315 AAAGATTTCAGAAATCGTGTTCATTTTGTAAACAAACCCCTGGCTGTGGCTTACTTGG 1374
 QY 1132 CAGCAATTGATGCTTGTTCAGAAATTTTCAGGGCCGTGGAGAAATGCTTTTGAAGATAA 1191
 DB 1375 CTGCTATTGATGCTTGTTCAGAAATTTTCAGGGCCGTGGAGAAATGCTTTTGAAGATAA 1434
 QY 1192 CAATTGAACCAATGCAATTCAGTTTCCAGTATTTGGCAGCGCTGCTGAGGGACCAAG 1251
 DB 1435 CCAATTGAACCAATGCAATTTCCAGTATTTGGCAGCGCTGCTGAGGGACCAAG 1494
 QY 1252 AGATCGTCTGACGGCTCAGCTGGCGCTTCTGATCTCTGCGAAGAGGGCGTGGCGC 1311
 DB 1495 AGATTGTGTGAATGGGACAAACCGTGTCTGATCTCTGCGAAGAGGGCGTGGCGC 1554
 QY 1312 CTCCTGCAAGAAATCATGTCAGACTCGCAAGCCACCGCCGAGCAGAGGGTCTCCATGGGG 1371
 DB 1555 CTCCTGCAAGAAATCATGTCAGACTCGCAAGTTCATGTCAGAAAGGGCTAACAAATGGGAA 1614
 QY 1372 AAAAGGGCTATGGCAGGGTGAAGAAATGTCATGAGCACCACCATGCTGAGAGATCG 1431
 DB 1615 AGAAAGGGTATGAAGAGTGAAGAGAGATTTCTGGAGCCCATATGTCGCGAGAAATG 1674
 QY 1432 CGCGCGTGTGAAGGATGCTTGGAGCAAAATTCACAGGA 1468
 DB 1675 CATTTGTTTGAAGGATTTTACAGAGGCTAAGCA 1711

RESULT 7

US-10-767-795-6175
 ; Sequence 6175, Application US/10767795
 ; Publication No. US20040181830A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Zhou, Yihua
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: Plants and Uses Thereof For Plant Improvement
 ; CURRENT APPLICATION NUMBER: US/10/767,795
 ; CURRENT FILING DATE: 2004-01-30
 ; NUMBER OF SEQ ID NOS: 117596
 ; SEQ ID NO 6175
 ; LENGTH: 1094
 ; TYPE: DNA
 ; ORGANISM: Gossypium hirsutum
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C7042_1
 US-10-767-795-6175

Query Match 25.0%; Score 426.2; DB 8; Length 1094;
 Best Local Similarity 65.0%; Pred. No. 6.1e-120;
 Matches 666; Conservative 0; Mismatches 348; Indels 11; Gaps 2;

QY 627 ATGCGTGGGCAATTAATTAAGTTGAATATGTCACAACTTCCCTTTGCTGGAGCC 686
 DB 13 ATGCGAGGCGCAATTTCTTAATTAATTAAGTATGTAAGATCATGCAACGCTGTATCTGGTGA 72
 QY 687 ATGATTGATTCTCATACAAACCGGTGAGTATTTGAATAGCA-----GGACTAGCGATCG 739
 DB 73 ATGATTGATTTCACCGTCACAGCGGAATATTGAAGATATCCACCGCGCGCCCGCG 132
 QY 740 CTTGAAATACAGATGCCCAAACTTATGTTGTTTACCTGGGGAAATAGTAAGAACTAAT 799
 DB 133 GCCGAAGATTAATAATGCTGAGACCTATGTTGTTTACCTTTGGAATAGCAATGAATGAT 192
 QY 800 GGAAGTTGCTGAAGACAAATGTCGCAAGAGAGTCTTACGGGAACATATTTCTGTAATCCCT 859

RESULT 8

US-09-923-876-6035
 ; Sequence 6035, Application US/09923876
 ; Patent No. US20020013958A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lalgudi, Raghunath V.
 ; APPLICANT: Kamigaki, Laura Y. (Ito)
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
 ; FILE REFERENCE: PL-0012-1 CON
 ; CURRENT APPLICATION NUMBER: US/09/923,876
 ; CURRENT FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: 09/298,329

DB 193 GCAAGTTCAGAGACAGTGTGGCTAAAGGGTTTTTGGTGAACATGTTTCGTGAATTCGCT 252
 QY 860 TGGAGTACGGAGTGAAGATCTCTCTGTTTGCATTAATAAACAGTGTATCAACGAGGAAGGG 919
 DB 253 TGGAGTGGCGCAATGACGATTTACTCTTTGCTTAAATAATAGTGTTCACGAGGAAAGG 312
 QY 920 ACAAGACTTATTTCTTCAAGCAATTTATCAGGCTTTGAGCTTCATCCAAACGAGAAACT 979
 DB 313 CAGGATCTCTTTCTACGGCTTTCTACGAGCCCTTACAACTGATCAAGCAAAAGAAAT 372
 QY 980 TAAAGTGCCTAGCAATACATGCTGTAGTTGTGGGAAGTGAATGTTAATGCTCAGACCAAT 1039
 DB 373 GCAGGTGCCACCAATTCATGCAATTAATTTCTGGAAGTGAATGAGTGGCGCATACGAACT 432
 QY 1040 TGAGACTCAGTTACGTGACTTTGTTGGTGAAGAACAGATTCATGACCGTGTCAATTTGT 1099
 DB 433 TGAATGGAATTAACGAGCTTATGTAACACAGAAAGAAATTCAGATCGTGTTCACCTTTGT 492
 QY 1100 GAACAGACATTTGGCAGTGGCCCTTACTTTGGCAGCAATTTGATGCTTGTTCAGAAATTC 1159
 DB 493 GAACAAAATCTTAAACAGTAGTCTCCATATTTAGTCCGCTAGATGTTCTTTTCAGAAATTC 552
 QY 1160 TCAGGGCCGTGAGAAATGCTTTTGAAGGATTAACAATTTGAAGCAATGGCAATTCAGTTGCC 1219
 DB 553 TCAGGGACGGGAGAAATGCTTTTGGACGATTAACAATTCGAAGCAATGGCAATTCAGTTGCC 612
 QY 1220 AGT-----ATTGGGACCGCTGCTGAGAGGACCAACGAGATTCCTCTGAGCGGTGCACTG 1275
 DB 613 TGTGCTGACAGGAAACAGCTGCGGGGGCACAAACGAAATAGTAGTGAAACGGCACAAACAG 672
 QY 1276 GCCTTCTGCATCTCTGGAAGAGGGCGTGGCGCTCTTGCAGAAACATCGTCAGAC 1335
 DB 673 GTTATTTGACCTCTGCGGAAAGAGGGGTGACAACTCTGCGGAAACATATTTGTGAAC 732
 QY 1336 TCGCAAGCCACCGCAGCAGAGGGGTCTCCATGGGGGAAAGGGCTATGCGAGGGTGAAGG 1395
 DB 733 TAGCTACGATCTAGAGAGAGGGCTTACAATAGGAAGAGAGGGTACGAAGGGTGAAG 792
 QY 1396 AAATGTTTCATGGAGACCAATCGCTGAGAGATCGCGCGGTGTTGAAGGATGCTCTGA 1455
 DB 793 AAAGATTTCTAGAACATCAATGCGAGAGAAATTTGGTGAAGTACTTAAAGAAAGCGTTGA 852
 QY 1456 GGAATTCAGAGCAGCACTCCAGTCTTGGAGCTTTGCGGTGCCCATCAGCTTGGCTTAACA 1515
 DB 853 GGAAGTCTTAAATCAGATCAAGTAAACACCTTTGACAGTGAACACCCCGCCACCATAA 912
 QY 1516 TGTGAACCTAGATTTTACGGGCTACGCCCTACCGTGTTCAGGCTGTAAACTGTAGATTGCA 1575
 DB 913 AATTACATGAGTATATCCAGTTTCAATCAATATATGAGTGAATCTTTTAAATCTG 972
 QY 1576 CTCTGTTGCTTACTTTTTCATTCATGTTTTTACCTATTAGCCCATGTCGATTTCTATT 1635
 DB 973 GCCTTTTCTTTCTTCT 1032
 QY 1636 CCAAT 1640
 DB 1033 ACAT 1037

; PRIOR FILING DATE: 1999-04-21
 ; PRIOR APPLICATION NUMBER: 60/085,331
 ; PRIOR FILING DATE: 1998-05-05
 ; NUMBER OF SEQ ID NOS: 6332
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 6035
 ; LENGTH: 276
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. US20020013958A1 700458234H1
 ; NAME/KEY: unsure
 ; LOCATION: 200, 275
 ; OTHER INFORMATION: a, t, c, g, or other
 US-09-923-876-6035

Query Match 15.4%; Score 262; DB 3; Length 276;

Best Local Similarity 99.3%; Pred. No. 1.3e-69;

Matches 273; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1034 CAAATTTGAGACTCAGTTACGTGACTTTGTGTGAAGAACACGATTTCATGACCGGTCCA 1093
 Db 1 CAAATTTGAGACTCAGTTACGTGACTTTGTGTGAAGAACACGATTTCATGACCGGTCCA 60
 QY 1094 TTTTGTGAACAAGACATTGGCAGTGGCCCCCTTACTTTGGCAGCAATTGATGCTTTGTCCA 1153
 Db 61 TTTTGTGAACAAGACATTGGCAGTGGCCCCCTTACTTTGGCAGCAATTGATGCTTTGTCCA 120
 QY 1154 GAATTTCTCAGGCGCGTGGAGAAATGCTTTGGAAAGGATAACAATTGAAGCAATGGCATTCAA 1213
 Db 121 GAATTTCTCAGGCGCGTGGAGAAATGCTTTGGAAAGGATAACAATTGAAGCAATGGCATTCAA 180
 QY 1214 GTTGCAGTATTGGCAGCGTCTGTGGAGGACACGAGATCGTCTGGAGCGCTCGAC 1273
 Db 181 GTTGCAGTATTGGCAGCGTCTGTGGAGGACACGAGATCGTCTGGAGCGCTCGAC 240
 QY 1274 TGGCCCTTCTGCATCTCTGCTGGGAAGGAGGCGTGG 1308
 Db 241 TGGCC-CTCTGCATCTCTGCTGGGAAGGAGGCGTGG 274

RESULT 9

; Sequence 6035, Application US/09923876
 ; Publication No. US20030237110A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Laligudi, Raghunath V.
 ; APPLICANT: Kamigaki, Laura Y. (Ito)
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
 ; FILE REFERENCE: PL-0012-1 CON
 ; CURRENT APPLICATION NUMBER: US/09/923,876
 ; CURRENT FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: 09/298,329
 ; PRIOR FILING DATE: 1999-04-21
 ; PRIOR APPLICATION NUMBER: 60/085,331
 ; PRIOR FILING DATE: 1998-05-05
 ; NUMBER OF SEQ ID NOS: 6332
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 6035
 ; LENGTH: 276
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. US20030237110A9 700458234H1
 ; NAME/KEY: unsure
 ; LOCATION: 200, 275
 ; OTHER INFORMATION: a, t, c, g, or other
 US-09-923-876-6035

Query Match 15.4%; Score 262; DB 3; Length 276;

Best Local Similarity 99.3%; Pred. No. 1.3e-69;
 Matches 273; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 1034 CAAATTTGAGACTCAGTTACGTGACTTTGTGTGAAGAACACGATTTCATGACCGGTCCA 1093
 Db 1 CAAATTTGAGACTCAGTTACGTGACTTTGTGTGAAGAACACGATTTCATGACCGGTCCA 60
 QY 1094 TTTTGTGAACAAGACATTGGCAGTGGCCCCCTTACTTTGGCAGCAATTGATGCTTTGTCCA 1153
 Db 61 TTTTGTGAACAAGACATTGGCAGTGGCCCCCTTACTTTGGCAGCAATTGATGCTTTGTCCA 120
 QY 1154 GAATTTCTCAGGCGCGTGGAGAAATGCTTTGGAAAGGATAACAATTGAAGCAATGGCATTCAA 1213
 Db 121 GAATTTCTCAGGCGCGTGGAGAAATGCTTTGGAAAGGATAACAATTGAAGCAATGGCATTCAA 180
 QY 1214 GTTGCAGTATTGGCAGCGTCTGTGGAGGACACGAGATCGTCTGGAGCGCTCGAC 1273
 Db 181 GTTGCAGTATTGGCAGCGTCTGTGGAGGACACGAGATCGTCTGGAGCGCTCGAC 240
 QY 1274 TGGCCCTTCTGCATCTCTGCTGGGAAGGAGGCGTGG 1308
 Db 241 TGGCC-CTCTGCATCTCTGCTGGGAAGGAGGCGTGG 274

RESULT 10

; Sequence 6078, Application US/09923876
 ; Patent No. US20020013958A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Laligudi, Raghunath V.
 ; APPLICANT: Kamigaki, Laura Y. (Ito)
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
 ; FILE REFERENCE: PL-0012-1 CON
 ; CURRENT APPLICATION NUMBER: US/09/923,876
 ; CURRENT FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: 09/298,329
 ; PRIOR FILING DATE: 1999-04-21
 ; PRIOR APPLICATION NUMBER: 60/085,331
 ; PRIOR FILING DATE: 1998-05-05
 ; NUMBER OF SEQ ID NOS: 6332
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 6078
 ; LENGTH: 257
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. US20020013958A1 700458322H1
 US-09-923-876-6078

Query Match 15.1%; Score 257; DB 3; Length 257;

Best Local Similarity 100.0%; Pred. No. 4.2e-68;

Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1035 AAAATTTGAGACTCAGTTACGTGACTTTGTGTGAAGAACACGATTTCATGACCGGTCCA 1094
 Db 1 AAAATTTGAGACTCAGTTACGTGACTTTGTGTGAAGAACACGATTTCATGACCGGTCCA 60
 QY 1095 TTTTGAACAAGACATTGGCAGTGGCCCCCTTACTTTGGCAGCAATTGATGCTTTGTCCA 1154
 Db 61 TTTTGAACAAGACATTGGCAGTGGCCCCCTTACTTTGGCAGCAATTGATGCTTTGTCCA 120
 QY 1155 AATTTCTCAGGCGCGTGGAGAAATGCTTTGAAGGATAACAATTGAAGCAATGGCATTCAA 1214
 Db 121 AATTTCTCAGGCGCGTGGAGAAATGCTTTGAAGGATAACAATTGAAGCAATGGCATTCAA 180
 QY 1215 TTGCAGTATTGGGACACGCGTCTGTGGAGGACACGAGATCGTCTGGAGCGCTCGACT 1274
 Db 181 TTGCAGTATTGGGACACGCGTCTGTGGAGGACACGAGATCGTCTGGAGCGCTCGACT 240
 QY 1275 GCGCTTCTGCATCTCTGCG 1291

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Db 241 GGCCTTCTGCATCCTGC 257

RESULT 11
US-09-923-876-6078
; Sequence 6078, Application US/09923876
; Publication No. US20030237110A9
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 6078
; LENGTH: 257
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030237110A9 700458322H1
US-09-923-876-6078

Query Match 15.1%; Score 257; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 4.2e-68;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1035 AATTGAGACTCAGTTAGCTGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCCAT 1094
Db 1 AATTGAGACTCAGTTAGCTGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCCAT 60
QY 1095 TTTGGAACAAGACATTTGGAGTGGCCCTTACTTGGAGCAATTGATGCTGTTCAG 1154
Db 61 TTTGGAACAAGACATTTGGAGTGGCCCTTACTTGGAGCAATTGATGCTGTTCAG 120
QY 1155 AATTCTCAGGGCGTGGAGATGCTTTGGAAGGATAACAAATGAAGCAATGGCAATCAAG 1214
Db 121 AATTCTCAGGGCGTGGAGATGCTTTGGAAGGATAACAAATGAAGCAATGGCAATCAAG 180
QY 1215 TTGCCAGTATTTGGACGGCTGCTGGAGGACCAACGAGATCGTCTGGACGGCTCGACT 1274
Db 181 TTGCCAGTATTTGGACGGCTGCTGGAGGACCAACGAGATCGTCTGGACGGCTCGACT 240
QY 1275 GGCCTTCTGCATCCTGC 1291
Db 241 GGCCTTCTGCATCCTGC 257

RESULT 12
US-10-767-795-3626
; Sequence 3626, Application US/10767795
; Publication No. US20040181830A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53534)B
; CURRENT APPLICATION NUMBER: US/10/767,795
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 117596
; SEQ ID NO 3626
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
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; FEATURE:
; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C6051_1
US-10-767-795-3626

Query Match 14.4%; Score 244.8; DB 8; Length 948;
Best Local Similarity 68.8%; Pred. No. 5.7e-64;
Matches 352; Conservative 0; Mismatches 157; Indels 3; Gaps 1;

QY 249 ACCGCCGTGCGCAGCGGAGTCCCTCGGTTTCATGAGGTCCCAAGCTCGTGTCTCTCGTC 308
Db 393 ATCGCGGCTGTGAAGCCGAGTCCGCTTAGCTTTATGAAGTCCACGCGTCCGCTGCTGGT 452
QY 309 TCCCATGAGCTCTCCCTCTCTGCTGCTCCACCTTTTACTGATGAAATAGCATTTCTTCG 368
Db 453 TCGCAGAGCTCTCGCTTTCTGTTGGACCAATGTTGCGGATGGAGCTGCGATTCCTATTA 512
QY 369 AGGCATGTTGGCTCGCAAGTGGTGGATATAACAAACCAAGATCAAGAAACAAATGAT 428
Db 513 AGAAGTGTGGTGTGAAGTTTATTGGATGACAAATATGAACCATCTGAACAGATGAA 572
QY 429 GTCACATATAGCTTGGAGCATAGGATGTTGAACCATGGAGTGCAGGTTTACCAGCTAGA 488
Db 573 GTAACATATAGTTTGAACATAAAGATGTTGGAAGAGGATACAGTTATCTCAGCTAAG 632
QY 489 GGACAGGAGGAGTGTGATATTGCTCTAAAAGCTGATCTGTTTATCTTAAACACTGCTGT 548
Db 633 GGGAAAGAGCTTTAGACTACTGCTTAAGAGCTGATTTGGTTGTTTGAACACTGCAATT 692
QY 549 GCTGCAAGTGGCTTGACCTGTTCTGAAAGATCATGTTCTTAAAGTCTCTCGGAAGATT 608
Db 693 GCTGGGAATGGCTGGATGTTCTTAAAGGAGATGTTTCATCGTGTCTGCTTAAGGTG 752
QY 609 TTGCTGGTGCATCATGAATGGTGGCAATTAATTTAGGTTGAATATCTCAACATCTT 668
Db 753 TTGCTGGTGCATCATGAATGGTGGCAATTAATTTAAATTAAGACTATGTAAGCAATCT 812
QY 669 CCCTTTGT---TGCTGGAGCCATGATTGATTTCTCATACAAACGGCTGAGTATTGGAATAGC 725
Db 813 TCTCTTTGTATCTGCTGCTATGATTGATTTCCATGTTTACACAGAACTACTGGAAGAT 872
QY 726 AGGATAGCGATCGCCTGAAATACAGATGCC 757
Db 873 AGTACTAAAGAACGTTTGAAGTTTAAATGTC 904

RESULT 13
US-09-770-152-133/c
; Sequence 133, Application US/09770152
; Publication No. US20020040489A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krieker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2025US (PARA-014PRV)
; CURRENT APPLICATION NUMBER: US/09/770,152
```

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; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,503
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-152-133

```

Query Match	13.7%	Score 233;	DB 3;	Length 583;
Best Local Similarity	66.3%;	Pred. No. 1.8e-60;		
Matches 335;	Conservative 0;	Mismatches 170;	Indels 0;	Gaps 0;
QY	963	ATCCACACAGAGAAACTTAAAGTCGCCCTAGAAATACATGCTCTAGTGTGGGAAGTGATGTT	1022	
DB	568	ATCAAAGAGAGAAACTTTCAGGTACCAACAAATGCAATGCTCAGTAGTAGTAGGAAGCGACATG	509	
QY	1023	AATGCTCAGACCAAAATTTGAGACTTCAGTTACGTGACCTTTCTGGTGAAGAACACGATTCAT	1082	
DB	508	AGCAAGCAGACAAGTTCGAGACAGAGCTACGCAACTTGTCCGAGAAAGAACTTGAG	449	
QY	1083	GACCGTGTCCATTTTGTGAACAAGACAAATGGCAGTGGCCCCCTTACTTTGGCAGCAATTGAT	1142	
DB	448	AACTTTGTCCACTTCGTCAACAAAACTCTAACCGTAGCACCATATATAGCAGCCATAGAC	389	
QY	1143	GTGCTTTGTTTCAGAAATTCAGGGCCGTGGAGAAATGCTTTTGGAGAGGATAACAATTGAGCA	1202	
DB	388	GTTCCTTGTCCAAACTCCCAAGCCAGAGGAGAAATGCTTTGGGAGAAATAACAATCGAAGCC	329	
QY	1203	ATGGCAATTCAAAGTTGCCAGTATTTGGGCA CGGCTGCTGGAGGGACCGAGAGATCGTCTCGT	1262	
DB	328	ATGGCCCTTTAAGCTACTCTGTACTTTGGTACTGACGCGGAGAACATGGAGATTGTAGTG	269	
QY	1263	GACGGTTCGACTCGGCCCTTTCGCAATCCCTGCTGGGAAAGGAGCGCGTGGCGCCTCTTTGCAAAG	1322	
DB	268	AAATGGAACGACTGGTCTGTTTACATAGTGCAGGGGAAAGAAAGAGTGATATCCTCTCGCCAAG	209	
QY	1323	AACATCGTCAGACTCCGCAAGCCAGCCGAGCAGAGGGTCTCCATGGGGGAAAGGGCTAT	1382	
DB	208	AACATAGTAGAATTGGCGACGCAAGTTGAGTTACGGCTGAGAAATGGGAAAAAATGGGTAT	149	
QY	1383	GGCAGGGTGAAGGAAATGTTTCATGGAGCACCAATGGCTCAGAGAGATCGCGGGGTGTTG	1442	
DB	148	GAGAGAGTAAAGAGATGTTTTTGGACATCATATGTTCACATCGAATAGTTCGGTACTC	89	
QY	1443	AAGGATGTCCTGAGGAAATCACAGG	1467	
DB	88	AAAGAAAGTCTTGCAAACACGCAAGG	64	

```

RESULT 14
US-10-021-323-13572
; Sequence 13572, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Peng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molec
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 6
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 13572
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Gossypium hirsutum

```

; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3829-012-Q6-K6-G10
 US-10-021-323-13572

Query Match	13.3%	Score 227;	DB 7;	Length 625;
Best Local Similarity	70.7%	Pred. No. 1.4e-58;		
Matches 302;	Conservative 0;	Mismatches 125;	Indels 0;	Gaps 0;
Qy	240	GCCTCAACACCGCGCTCGCGAGGAGTCCCTCGGGTTTCATGAGGTCCAAAGCTCGTG	299	
Db	199	GCCTCAACACCGCGCTCGCTGCAAGCGAGTCCACTCAGTTTTCATGAAGTCCAAAGATTGTT	258	
Qy	300	CTCCTCGTCTCCCATGAGCTCTCCTCTCTGCTGCTCCACTTTTCTGATGGAATTAGCA	350	
Db	259	CTACTGCTGCGCACGAGCTCTCGCTTCTGCTGCGACCATTTGTTGATGGAGGTAGCA	318	
Qy	360	TTTCTTCTGAGGCGATGTTGGCTCGCAAGTGGTGTGGATAACAAACACAGAGATCACAAGAA	419	
Db	319	TTTCTATTAGAAGTGTGGTCTGAGTTAAATGGGTTACATTATGAACCATCTGAA	378	
Qy	420	ACAAATGATGTCATATATAGCTTTGGAGCATPAGAGATGTTGAACCATGGAGTGCAGGTTTAA	479	
Db	379	ACTGATGAAGTAATATATAGTTTTAGAACATAGAATGTTGGACAGAGAGTGCAGGTTTTC	438	
Qy	480	CCAGCTAGAGGACAGAGGCGAGTTGATATGCTCTCAAAAGCTGATCTGGTTTATCTCTAAAC	539	
Db	439	TCCGCGTTTGGAAAGAGCTATAGATATGCTCTTAAGAGCTGATTTGGTTGTTTGAAC	498	
Qy	540	ACTGCTGTTGCTGGCAAGTGGCTTGACCCCTGTTCTTGAAAGATCATGTTTCTTAAAGTCCCT	599	
Db	499	ACAGCGGTTGCTGGGAAATGGGTAGATTATGTTCTTTAAGGAAGATATTCACCGGTGTTCTG	558	
Qy	600	CCGAGATTTTGGTGGATCCATGAAATCGGTGGGCATTACTTTAAGGTTTGAATATGTC	659	
Db	559	CCTAAGTGTGTGGTGGATCCATGAATGCGAGGCCATTACTTCAATTTAGAGTATGTA	618	
Qy	660	AAACATC	666	
Db	619	AAGCATC	625	

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RESULT 15
US-10-767-795-3627
, Sequence 3627, Application US/10767795
, Publication No. US20040181830A1
, GENERAL INFORMATION:
, APPLICANT: Kovalic, David K.
, APPLICANT: Cao, Yongwei
, APPLICANT: Zhou, Yinwei
, TITLE OF INVENTION: Nucleic Acid Molecule
, TITLE OF INVENTION: Plants and Uses Thereof
, FILE REFERENCE: 38-21(53534)B
, CURRENT APPLICATION NUMBER: US/10/767,795
, CURRENT FILING DATE: 2004-01-30
, NUMBER OF SEQ ID NOS: 117596
, SEQ ID NO 3627
, LENGTH: 625
, TYPE: DNA
, ORGANISM: Gossypium hirsutum
, FEATURES:
, OTHER INFORMATION: Clone ID: LIEB3829-012
US-10-767-795-3627

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	Best Local Similarity	70.7%;	Pred. No. 1.4e-58;		
	Matches 302;	Conservative 0;	Mismatches 125;	Indels 0;	Gaps 0;
Qy	240	GCCTCAACACGGCGTCCGACGGGAGTCCCTCGGGTTCATGAGTCCAGCTCGTG	299		
Db	199	GCCTCCGAGATCGTCTGCAAGCGGAGTCCACTAGTTCATGAAGTCCAGATTGTT	258		
Qy	300	CTCCTCGTCTCCCATGAGCTCTCCCTCTCTGGTGGTCCACTTTTACTGATGGAAATTAGCA	359		

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Db      259 CTACTGGTTCGCACGAGCTTCGCTTTCTGCTGGACCAATTGTTGTTGATGGAGCTAGCA 318
Qy      360 TTTCTTCTGAGGCATGTTGGCTCGCAAGTGGTGGATACAAACACGAGATCAACAGAA 419
Db      319 TTTCTATTAAAGAAGTCTTGGTCTGAAGTTAAATTGGGTTACATTTATGAAACCATCTCAA 378
Qy      420 ACAATATGATGTCACATATAGCTTGGAGCATAGGATGTTGAACCATGCGAGTGCAGGTTTTA 479
Db      379 ACTGATGAAGTAAATATATAGTTTGAACATAAGATGTTGGACAGAGGAGTGCAGGTTTTC 438
Qy      480 CCAGCTTAGAGGACAGGAGGCGAGTTGATATTGCTCTAAAGCTGATCTGTTATCTTAAAC 539
Db      439 TCCGCGTTTGGAAAGAAGCTATAGATACTGCTCTAAGAGCTGATTTGGTGTGTTTGAAC 498
Qy      540 ACTGCTGTTGCTGGCAAGTGGCTTGACCCCTGTTCTGAAAGATCATGTTCTTAAAGTCCTT 599
Db      499 ACAGCGGTTGCTCGGAAATGGGTAGATTATGTTCTTAAAGAAAGATATTCACCGTGTCTG 558
Qy      600 CCGAAGATTTTGTGTGGATCCATGAATGCGTGGGCATTACTTTAAGGTTGAATATGTC 659
Db      559 CCTAAGGTGTTGTGTGGATCCATGAATGCGAGGCCATTACTTCAATTAGAGTATGTA 618
Qy      660 AAACATC 666
Db      619 AAGCATC 625

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 Job time : 1458 secs

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OM nucleic - nucleic search, using sw model

Run on: March 17, 2006, 05:11:45 ; Search time 1626 Seconds
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Title: US-09-938-294-2

Perfect score: 1702

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Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq.*
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- 7: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq.*
- 8: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq.*
- 9: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
- 12: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
- 13: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	48.6	2.9	172543	12 US-11-121-086-6	Sequence 6, Appli
C 2	46.6	2.7	1621	9 US-11-096-568A-19793	Sequence 19793, A
C 3	46.4	2.7	23187	9 US-11-236-198-1	Sequence 1, Appli
C 4	46.2	2.7	1019	9 US-11-096-568A-2921	Sequence 2921, Ap
C 5	46.2	2.7	5706	12 US-11-052-554A-519	Sequence 519, App
C 6	45.6	2.7	68741	7 US-10-330-773-26	Sequence 26, Appl
C 7	45.4	2.7	1218	9 US-11-096-568A-12913	Sequence 12913, A
C 8	44.6	2.6	3921	12 US-11-052-554A-523	Sequence 523, App
C 9	44.4	2.6	1362	9 US-11-096-568A-25661	Sequence 25661, A
C 10	44.4	2.6	2954	12 US-11-241-347-2	Sequence 2, Appli
C 11	44	2.6	100000	12 US-11-124-367A-5048	Sequence 5048, Ap
C 12	43.8	2.6	2187	9 US-11-245-147-141	Sequence 141, App
C 13	43.6	2.6	1263	7 US-10-016-686-14	Sequence 14, Appl
C 14	43.4	2.5	7006	8 US-10-821-234-218	Sequence 218, App
C 15	43.4	2.5	10968	12 US-11-075-185-35	Sequence 35, Appl
C 16	43.4	2.5	78869	12 US-11-075-185-1	Sequence 1, Appli
C 17	43	2.5	1147	9 US-11-096-568A-4612	Sequence 4612, Ap
C 18	43	2.5	1580	9 US-11-096-568A-25769	Sequence 25769, A
C 19	42.8	2.5	984	9 US-11-096-568A-10550	Sequence 10550, A
C 20	42.8	2.5	2000	12 US-11-156-084-364	Sequence 364, App

ALIGNMENTS

RESULT 1

US-11-121-086-6/c

; Sequence 6, Application US/11121086

; Publication No. US20050266459A1

; GENERAL INFORMATION:

; APPLICANT: POULSEN, TIM S.

; APPLICANT: NIELSEN, KIRSTEN V.

; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

; FILE REFERENCE: 09138.6000-00000

; CURRENT APPLICATION NUMBER: US/11/121,086

; CURRENT FILING DATE: 2005-05-04

; PRIOR APPLICATION NUMBER: 60/567,570

; PRIOR FILING DATE: 2004-05-04

; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 6

; LENGTH: 172543

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-121-086-6

Query Match 2.9%; Score 48.6; DB 12; Length 172543;

Best Local Similarity 50.2%; Pred No. 0.029;

Matches 146; Conservative 0; Mismatches 144; Indels 1; Gaps 1;

QY 34 CTCCTCGGCGCCACCGGTCGCGGATGCGAAGACCGCGTTCGTCGCGGTGGCGG 93

Db 109633 CTCACCGGCGCGCGGCTTCCAGCGGCGCGCCCAAGCGCGGCAAGAGCGCGCAG 109574

QY 94 CGGTGCGCGGAGCGCGCGGTCGCGGATGCGGACCGCGCTCTCTCTCTCTCTCTCT 153

Db 109573 CGGCGCGCAACACGCGGAGGACCGCGCGGTCGCGGCGCGCC-CGCGCTCA 109515

QY 154 TGGCGGTGCGACGCTCGCGATCCACAGAGGGTTCCTCTCGCGGTGCGCTCGAGACC 213

Db 109514 CGGCTTCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGGGGGGG 109455

QY 214 CTTGGAGCGCGCGTGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGTCCCC 273

Db 109454 CTTGCTCG 109395

QY 274 TCGGGTTCATGAGGTTCAGCTCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 324

Db 109394 CGCTCCCAAGGAGCGCGGCTCGCCCTCTCCGGGCTCCACGGCGCGCGC 109344

RESULT 2

US-11-096-568A-19793
 ; Sequence 19793, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nikolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 ; FILE OF INVENTION: Therby
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO 19793
 ; LENGTH: 1621
 ; TYPE: DNA
 ; ORGANISM: Zea mays subsp. mays
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(1621)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12374562
 US-11-096-568A-19793

Query Match 2.7%; Score 46.6; DB 9; Length 1621;
 Best Local Similarity 49.8%; Pred. No. 0.0092;
 Matches 118; Conservative 0; Mismatches 119; Indels 0; Gaps 0;
 QY 92 GCGGTCGCGGAGCGCGGCGGTTCAACACGGAGCCAGCTCTCTCTCTCTCT 151
 Db 535 GCGGTACGCGCGCGCGCGCGCTCGGACTCTGGCTACTTCTCTCTGACGT 594
 QY 152 CBTGCGCGTCGACAGCTCGGCATCCACAGCAGGGTTCTCTCCGCGGTGCCCTGCAGA 211
 Db 595 GCGGCGCTTCGCGCTCGTCGCGCTCAAGCTCTTCGCGTCCGCGAGCCACCGCT 654
 QY 212 CCTTCGAGCGCGGTGGGACCCCGCGCTCAACACGGCGGTGCCAGCGGAGTCC 271
 Db 655 CAAGTTCTCGGAGCGTCTGCTCGCTCTCTCATGCGCGTCTGTCGCGCGCTCAG 714
 QY 272 CBTGCGGTTCATGAGTCCAAAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTC 328
 Db 715 CATCATCGTCAAGTGTCAAGACCAAGAGCGTCAAGTTCTCTGCCCATGAGCTCTC 771

RESULT 3

US-11-236-198-1
 ; Sequence 1, Application US/11236198
 ; Publication No. US20060030530A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yen, Frances
 ; APPLICANT: Erickson, Mary Ruth
 ; APPLICANT: Truebis, Joachim
 ; APPLICANT: Bihaun, Bernard
 ; TITLE OF INVENTION: Methods Of Screening For Compounds That Modulate the
 ; TITLE OF INVENTION: LSR-Leptin Interaction and Their use in the Prevention
 ; TITLE OF INVENTION: and Treatment of Obesity-Related Diseases
 ; FILE REFERENCE: 70.US2.REG
 ; CURRENT APPLICATION NUMBER: US/11/236,198
 ; CURRENT FILING DATE: 2005-09-27
 ; PRIOR APPLICATION NUMBER: US/09/668,558
 ; PRIOR FILING DATE: 2000-09-22
 ; PRIOR APPLICATION NUMBER: 60/155,506
 ; PRIOR FILING DATE: 1999-09-22
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 1
 ; LENGTH: 23187
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 2001..2356
 ; OTHER INFORMATION: exon1
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 3540..3884
 ; OTHER INFORMATION: exon2
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 12163..12282
 ; OTHER INFORMATION: exon3
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 15144..15200
 ; OTHER INFORMATION: exon4
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 15765..15911
 ; OTHER INFORMATION: exon5
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 19579..19752
 ; OTHER INFORMATION: exon6
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 19899..19958
 ; OTHER INFORMATION: exon7
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 20056..20187
 ; OTHER INFORMATION: exon8
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 20329..20957
 ; OTHER INFORMATION: exon9
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 21047..21187
 ; OTHER INFORMATION: exon10
 ; FEATURE:
 ; NAME/KEY: polyA signal
 ; LOCATION: 21168..21173
 ; OTHER INFORMATION: AATAAA
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1..2000
 ; OTHER INFORMATION: potential 5'regulatory region
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 22324..23187
 ; OTHER INFORMATION: homology with USP2 gene in ref: embl Y07661
 ; FEATURE:
 ; NAME/KEY: primer_bind
 ; LOCATION: 523..544
 ; OTHER INFORMATION: upstream amplification primer 17-2
 ; FEATURE:
 ; NAME/KEY: primer_bind
 ; LOCATION: 1047..1068
 ; OTHER INFORMATION: downstream amplification primer 17-2, complement
 ; FEATURE:
 ; NAME/KEY: primer_bind
 ; LOCATION: 946..963
 ; OTHER INFORMATION: upstream amplification primer 99-4576
 ; FEATURE:
 ; NAME/KEY: primer_bind
 ; LOCATION: 1385..1402
 ; OTHER INFORMATION: downstream amplification primer 99-4576, complement
 ; FEATURE:
 ; NAME/KEY: primer_bind
 ; LOCATION: 1096..1115
 ; OTHER INFORMATION: upstream amplification primer 9-19
 ; FEATURE:
 ; NAME/KEY: primer_bind
 ; LOCATION: 1616..1635


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; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..11019)
; OTHER INFORMATION: Ceres Seq. ID no. 14309484
US-11-096-568A-2921

Query Match      2.7%; Score 46.2; DB 9; Length 1019;
Best Local Similarity 51.2%; Pred. No. 0.0094;
Matches 108; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Qy      73  CCCGTCGTTCCGGTCGGCGGTGCGCGAGGCGCGGGCGCGGTTTCACAAACCGGACCC 132
Db      219  CCACGCTCGGGCGCTCCACGCGCCCGCTCACCACTACCTCAGCCTGCACGAGGGGATCC 278

Qy      133  AGCTTCCTCCTCCTCCTCTCGTCGCGCGAGCTCCGCGATCCACACGACGAGGTTTCCTCC 192
Db      279  ACTAGGCCCTCCTCGTCACCGTCTCCATCTTCGCGCTCCTCCTCTTCGCTTCAACCTCC 338

Qy      193  TCCGCGGTGCCCTCGAGACACCTTTGCGACGGCCGTTGGGGACCCCGCGCCCTTCAACACCG 252
Db      339  TCTCGACGCCCTCGCGGGCGCCAGTTCAACCCACCGCGCTGCGCGCTTCTACGCGG 398

Qy      253  CCGTGGCCAGGGAGTCCCCTCGGGTTCAT 283
Db      399  CCGGCTTACCAGCCCTCGCTCTTCTCCAT 429

RESULT 5
US-11-052-554A-519/c
; Sequence 519, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589, 227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 519
; LENGTH: 5706
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-519

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Query Match	2.7%	Score 46.2;	DB 12;	Length 5706;
Best Local Similarity	52.9%;	Pred. No. 0.023;		
Matches	99;	Conservative 0;	Mismatches 88;	Indels 0; Gaps 0;
Qy	91	CGCGGGTCGCGGAGCGCGGGCCGGTTCACAAACCGGACCCAGCTCTCTCTCTCTCTCTCC	150	
Db	1592	CCGGTGGCGCGCGTGGACCGGTAGCGGTTCGATCCGTGCGGGCTGCGCGGCGCCG	1533	
Qy	151	TCGTGGCGGTGCGAGCTTCGCGCATCCACAGAGGGTTCTCTCTCCGCGGTGCCCTGCGAG	210	
Db	1532	CGCGCGCTTTGGCGCGCGGTGCCGCCGATACCGGCTTGGCGCGGCGCGCAACCCCG	1473	
Qy	211	ACCCTTCGGAGCGCGGTGGGACCCCGCGCCCTCAACACGCGCGTCCGACGCGGGAGTC	270	
Db	1472	CCGGTTCCTCCGGTGC CGCGGCCCCCGCGGCCCCCGCGGCGCGGTTACCCCGATC	1413	
Qy	271	CCCTCGG	277	
Db	1412	CCACCG	1406	

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RESULT 6
US-10-330-773-26/c
; Sequence 26, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 687411
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(687411)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-26

Query Match      2.7%; Score 45.6; DB 7; Length 687411;
Best Local Similarity 50.5%; Pred.No. 0.44;
Matches 111; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

Qy      36  C C T C G G G C C C A C C G G T C C G A C C G C G A T G G C A A A G A C C C G T C G T T C G C G G T G C G C G C G 95
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Qy      96  G T C C C G G A G G C G G G G C G G T T C A C A A C G G A C C C A G C T C T C T C T C T C T C T C T C T G T 155
Db      48474  C G G C C C C C G C G G C G C G C G C G C A C G C G C C C C C C C A C A C C C C C G C C C C G C C C C G 48415

Qy      156  G C G T C G A C C T C C G A T C A C A C A C A G G T T C T C T C T C C G G G T C C C T G C G A G A C C C T 215
Db      48414  C C A C C G C G C A C C G C C C C C C C C C C C C G G G G C C C C G C C C C C G A A G A C C G C C G C G C C C 48355

Qy      216  T G C A G C G G C G T G G G A C C C C C C C C C C T C A A C A C C G C G 255
Db      48354  C G C C C C C C G C G C C C C C G C G C C C C C C C C C C C C C C C C G C C G C C C G C C C G 48315

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RESULT 7
US-11-096-568A-12913
; Sequence 12913, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 12913
; LENGTH: 1218
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1218)
; OTHER INFORMATION: Ceres Seq. ID no. 14313358
US-11-096-568A-12913

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	Query Match	2.7%	Score 45.4;	DB 9;	Length 1218;
	Best Local Similarity	49.4%;	Pred. No. 0.018;		
	Matches 118;	Conservative	0;	Mismatches 121;	Indels 0; Gaps 0
QY	90	GC	GC	GC	GC
DB	386	GT	GT	GT	GT

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Result No.	Query			DB	ID	Description
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C	1	1045.8	61.4	1449	10	CL1958234
	2	819.6	47.2	508	6	CD437062
	3	815.4	48.9	843	4	AY107383
C	4	753.8	44.3	758	8	DR802416
	5	752.4	44.2	752	8	DR790488
	6	732.4	43.0	732	8	DR805336
C	7	730.4	42.9	730	8	DR802415
	8	698.2	41.0	715	8	DR790489
	9	667.3	39.2	676	8	DN475283
C	10	659.4	38.7	879	6	CA184773
	11	656.8	38.6	831	6	CB661667
	12	650.2	38.2	675	6	CD435900
C	13	645.8	37.9	813	6	CB660163
	14	635.8	37.4	753	7	CD448834
	15	621.3	36.5	629	8	DR805335
C	16	615.36	36.1	615	4	AY108864
	17	614.2	36.1	667	6	CD222893
	18	593.4	34.9	810	8	AX067129
C	19	593.4	34.9	810	8	CX615619
	20	571.3	33.5	622	6	CD228925
	21	568.8	33.4	620	6	CD226599
C	22	554.2	32.5	819	6	CB660162
	23	554.2	32.5	819	6	CB660162
	24	554.2	32.5	819	6	CB660162

Db 848 CGGGAACATATTCGTGAATCCC-TGGAGTACGGAGTGGAGTCTCTCTGTTTCAATAATA 790
 Qy 897 AACAGTGTATCAGGAGGAAGGACAAAGACTTATTTCTTCAAGCATTTTATCAGGCTTTG 956
 Db 789 AACAGTGTATCAGGAGGAAGGACAAAGACTTATTTCTTCAAGCATTTTATCAGGCTTTG 730
 Qy 957 CAGCTCATCAACACAGAGAACTTAAAGTGCCTAGAAATACATCTGTAGTGTGGGAAGT 1016
 Db 729 CAGCTCATCAACACAGAGAACTTAAAGTGCCTAGAAATACATCTGTAGTGTGGGAAGT 670
 Qy 1017 GATGTTAAGTCTCAGACCAATTTGAGACTCAGTACGTGACTTGTGTGAGAACAGC 1076
 Db 669 GATGTTAAGTCTCAGACCAATTTGAGACTCAGTACGTGACTTGTGTGAGAACAGC 610
 Qy 1077 ATTATGACCGTGTCCATTTTGTGAACAAGACATTTGGCAGTGGCCCTTACTTGGCAGCA 1136
 Db 609 ATTATGACCGTGTCCATTTTGTGAACAAGACATTTGGCAGTGGCCCTTACTTGGCAGCA 550
 Qy 1137 ATTATGACCGTGTCCATTTTGTGAACAAGACATTTGGCAGTGGCCCTTACTTGGCAGCA 1196
 Db 549 ATTATGACCGTGTCCATTTTGTGAACAAGACATTTGGCAGTGGCCCTTACTTGGCAGCA 490
 Qy 1197 GAAGCAATGGCATTCAAGTTGCCAGTATTTGGGACCGCTGCTGGAGGACCAAGGAGATC 1256
 Db 489 GAAGCAATGGCATTCAAGTTGCCAGTATTTGGGACCGCTGCTGGAGGACCAAGGAGATC 430
 Qy 1257 GTCTCGACCGCTCGACTGCGCTTCTGCAATCTCTGCGGAAGAGGCGCTGCGCTCTTT 1316
 Db 429 GTCTCGACCGCTCGACTGCGCTTCTGCAATCTCTGCGGAAGAGGCGCTGCGCTCTTT 370
 Qy 1317 GCAAGAAACATCGTACAGACTCGCAAGCCAGCGGAGCAGAGGCTCTCCATGGGGGAAAG 1376
 Db 369 GCAAGAAACATCGTACAGACTCGCAAGCCAGCGGAGCAGAGGCTCTCCATGGGGGAAAG 310
 Qy 1377 GGTATGAGGAGGTGAAGAAATGTTTCATGAGACCAACATGGCTGAGAGATTCGGCGG 1436
 Db 309 GGTATGAGGAGGTGAAGAAATGTTTCATGAGACCAACATGGCTGAGAGATTCGGCGG 250
 Qy 1437 GTGTTGAAGGATCTCTGAGGAAATCAGAGGAGCAGCTCCAGGCTTTGAGCTTTCGGCTG 1496
 Db 249 GTGTTGAAGGATCTCTGAGGAAATCAGAGGAGCAGCTCCAGGCTTTGAGCTTTCGGCTG 190
 Qy 1497 CCATCAGCTTGGCTTAACATGTTGAATCTAGATTTTACGGGCTACGCTACGTTGTTT 1556
 Db 189 CCATCAGCTTGGCTTAACATGTTGAATCTAGATTTTACGGGCTACGCTACGTTGTTT 130
 Qy 1557 CTGTAACTGTAGATTGCACTCTGTTGGTCTACTTTTTCACATTC 1608
 Db 129 CTGTAACTGTAGATTGCACTCTCTTGGTCTACTTTTTCACATTCATTTTGTCTTT 70
 Qy 1609 ACCTATTAGGCAATGTCGATTTCTATTCCAAATTCATATAG 1648
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 ACCESSION AY107383
 VERSION AY107383.1 GI:21210461
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 SOURCE Zea mays
 ORGANISM Zea mays
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 843)
 REFERENCE
 AUTHORS Gardiner, J., Schroeder, S., Polacco, M.L., Sanchez-Villeda, H.,
 Fang, Z., Morgante, M., Landewe, T., Fengler, K., Useche, F.,
 Hanafey, M., Tingey, S., Chou, H., Wing, R., Soderlund, C. and Coe, E.H.
 Jr.

TITLE Anchoring 9,371 maize expressed sequence tagged unigenes to the bacterial artificial chromosome contig map by two-dimensional overgo hybridization
 JOURNAL Plant Physiol. 134 (4), 1317-1326 (2004)
 PUBMED 15020742
 REFERENCE 2 (bases 1 to 843)
 AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whiteitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
 TITLE Zea Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
 JOURNAL Unpublished (2002)
 REFERENCE 3 (bases 1 to 843)
 AUTHORS Coe, E.H.
 JOURNAL Direct Submission
 COMMENT Submitted (25-APR-2002) Zea Mapping Project, University of Missouri, Columbia, MO 65211, USA
 If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizeimap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
 FEATURES
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 /clone_lib="Maize Mapping Project/DuPont Consensus Library"
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 ORIGIN
 Query Match 47.9%; Score 815.4; DB 4; Length 843;
 Best Local Similarity 99.2%; Pred. No. 6.1e-219;
 Matches 827; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
 Qy 19 CCGAGCCCAACAGTCTCTCTCGGCCCCACCGCTCGAGCCGCGATGGCAAGACCCCGT 78
 Db 10 CGAGCCCAACAGTCTCTCTCGGCCCCACCGCTCGAGCCGCGATGGCAAGACCCCGT 69
 Qy 79 CGTTCCGGTGGCGGGTGGCGGAGCGCGGGCGGTTTCCACACCGGATCCAGCTCC 138
 Db 70 CGTTCCGGTGGCGGGTGGCGGAGCGCGGGCGGTTTCCACACCGGATCCAGCTCC 129
 Qy 139 TCCT 198
 Db 130 TCCT 189
 Qy 199 GTGCCCTCGAGACCCCTTTCGAGCGCGGTGGGAGACCCCGCCCTTCAACACCGCGCTG 258
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 Qy 319 TCCT 378
 Db 310 TCCT 369
 Qy 379 GCTCGCAAGTGTGTGGATTAACAAACAGAGATCAAGAGAAACAAATGATGACATATA 438
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 Qy 439 GCTTGAGCATAGGATGTTGAACCATGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 498

Db 430 GCTTGGAGCATAGGATGTTGAACCATGGAGTGCAGGTTTTCACAGCTAGAGCAGGAGG 489
 Qy 499 CAGTTGATATTCCTTAAAGCTGATCTGTTATCTTAAACACTGCTGTGTGCGCAAGT 558
 Db 490 CAGTTGATATTCCTTAAAGCTGATCTGTTATCTTAAACACTGCTGTGTGCGCAAGT 549
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 Db 550 GCCTTGACCTGTTCTGGAAGATCATGTTCTTAAAGTCTTCCGAAGATTTTGTGTGGA 609
 Qy 619 TCCATGAATGGTGGGCAATTAATTAAGTGTGAATATGTCAAACATCTTCCCTTTGTTG 678
 Db 610 TCCATGAATGGTGGGCAATTAATTAAGTGTGAATATGTCAAACATCTTCCCTTTGTTG 669
 Qy 679 CTGGAGCCATGATGATTTCTCATACACGGCTGATTTGGAATAGCAGGACTAGGCATC 738
 Db 670 CTGGAGCCATGATGATTTCTCATACACGGCTGATTTGGAATAGCAGGACTAGGCATC 729
 Qy 739 GCTGTAATAACAGATGCCACAACTTATGTTGTTTCCCTGGGGAATAGTAAAGAACTAA 798
 Db 730 GCTGTAATAACAGATGCCACAACTTATGTTGTTTCCCTGGGGAATAGTAAAGAACTAA 789
 Qy 799 TGGAGTTGCTGTAAGACAAAT-GTGCACAAGAGTCTTACGGGAACATATTCGT 851
 Db 790 TGGAGTTGCTGTAAGACAAAGGTGCGCAAGAGTCTTACGGGAACATATTCGT 843

RESULT 4

DR802416

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

ciade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 758)

Kim H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.

Maize Full-length cDNA Project

Unpublished (2005)

Contact: Yeisoo Yu

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Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu

Plate: 0026 row: K column: 16.

Location/Qualifiers

1..758

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="B73"

/db_xref="taxon:4577"

/issue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"

/dev_stage="varies by tissue"

/lab_host="DH10B T1 phage resistant"

/clone_lib="ZM_BFB"

/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, for permitting clone movement to new vector backbones, for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for

FEATURES

source

selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>).

ORIGIN

Query Match 44.3%; Score 753.8; DB 8; Length 758;
 Best Local Similarity 99.6%; Pred. No. 1.6e-201;
 Matches 755; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 30 GTCTCTCTCGGGCCACCGGCTCCGACCGGCGATGGCAAGACCCCGTCGTTCGGCGTG 89
 Db 1 GTCTCTCTCGGGCCACCGGCTCCGACCGGCGATGGCAAGACCCCGTCGTTCGGCGTG 60

Qy 90 GCGGCGGTGCGCGGAGGCGCGGGCGGTTTCAACACCGGACCCAGCTCTCTCTCTCTC 149
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Qy 150 CTCGTGGCGGTGCGCGACCTCCGATCCACAGCAGGCTTCCTCTCTCGCGGTGCGCTTCCCA 209
 Db 121 CTCGTGGCGGTGCGCGACCTCCGATCCACAGCAGGCTTCCTCTCTCGCGGTGCGCTTCCCA 180

Qy 210 GACCTTTCGACCGCGGTGGGACCCCGCGCTTCAACACCGCGCTCCGACGCGGAGT 269
 Db 181 GACCTTTCGACCGCGGTGGGACCCCGCGCTTCAACACCGCGCTCCGACGCGGAGT 240

Qy 270 CCGCTCGGGTTCATGAGGTCCAGCTCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 329
 Db 241 CCGCTCGGGTTCATGAGGTCCAGCTCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300

Qy 330 GGTGTGTCACATTTTACTGATGGAATTAGCATTTTCTTGAGGCATGTTGGCTCGCAAGTG 389
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Qy 390 GTGTGGATAACAAACACAGAGATCAACAGAAACAAATGATGTACATATAGTTGGAGCAT 449
 Db 361 GTGTGGATAACAAACACAGAGATCAACAGAAACAAATGATGTACATATAGTTGGAGCAT 420

Qy 450 AGGATGTTGAACCATGGAGTGCAGGTTTTACAGCTAGAGGACGAGGCGAGTTGATATT 509
 Db 421 AGGATGTTGAACCATGGAGTGCAGGTTTTACAGCTAGAGGACGAGGCGAGTTGATATT 480

Qy 510 GCTCTAAAAGCTGATCTGGTTATCTTAAACACTGCTGTTGCTGGCAAGTGGCTTGACCCCT 569
 Db 481 GCTCTAAAAGCTGATCTGGTTATCTTAAACACTGCTGTTGCTGGCAAGTGGCTTGACCCCT 540

Qy 570 GTTCTGAAAGATCATGTTCTCTAAAGTCTTCCGAAGATTTTGTGGTGGATTCATGAAATG 629
 Db 541 GTTCTGAAAGATCATGTTCTCTAAAGTCTTCCGAAGATTTTGTGGTGGATTCATGAAATG 600

Qy 630 CTGGGCGATTACTTTAAGGTTGAAATATGTCAACACTCTTCCCTTTGTTGCTGGAGGCATG 689
 Db 601 CTGGGCGATTACTTTAAGGTTGAAATATGTCAACACTCTTCCCTTTGTTGCTGGAGGCATG 660

Qy 690 ATTGATTTCTCATACACCGCTGAGTATTGGAATAGCAGGACTAGCGATCGCTTGAATAA 749
 Db 661 ATTGATTTCTCATACACCGCTGAGTATTGGAATAGCAGGACTAGCGATCGCTTGAATAA 720

Qy 750 CAGATGCCACAAACTATGTTGTTTCCCTGGGGAATAG 787
 Db 721 CAGATGCCACAAACTATGTTGTTTCCCTGGGGAATAG 758

ORIGIN

Email: yeisoo@genome.arizona.edu
 Plate: 0030 row: M column: 17.
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 /organism="Zea mays"
 /mol_type="mRNA"
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 /note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 day aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 day whole seed; 11. 12 day endosperm and embryo; 12. 17 day endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>)."

FEATURES
 source

ORIGIN

Query Match 43.0%; Score 732; DB 8; Length 732;
 Best Local Similarity 100.0%; Pred. No. 2.4e-195; Mismatches 0; Indels 0; Gaps 0;
 Matches 732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 37 CTCGGGCCACCGCGTCCGACCGCGGATGCAAGACCCCGTTCGCGGTGGCGCGG 96
 Db 1 CTCGGGCCACCGCGTCCGACCGCGGATGCAAGACCCCGTTCGCGGTGGCGCGG 60
 QY 97 TCGCCGGAGCCCGCGGCGGTTTCAACCGGACCCAGCTCTCTCTCTCTCTCTCTCT 156
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 QY 157 CCGTCGAGCTCCGATCCACAGCAGGGTTCTCTCTCGCGGTGCGCTCCGAGACCCCTT 216
 Db 121 CCGTCGAGCTCCGATCCACAGCAGGGTTCTCTCTCGCGGTGCGCTCCGAGACCCCTT 180
 QY 217 GCGACGCGCGTGGGACCCCGCGGCTCAACACCGCGGTGCGACGGGAGTCCCTCG 276
 Db 181 GCGACGCGCGTGGGACCCCGCGGCTCAACACCGCGGTGCGACGGGAGTCCCTCG 240
 QY 277 GGTTCATGAGTCCAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 336
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 Db 301 CACTTTTACTGATGGAATTAGCATTTCTCTGAGGATGTTGGCTCGCAAGTGGTGGGA 360
 QY 397 TAAACAAACAGAGATCAACAAACAAATGATGTCAATATAGCTTGGAGCATAGATGT 456
 Db 361 TAAACAAACAGAGATCAACAAACAAATGATGTCAATATAGCTTGGAGCATAGATGT 420

QY 457 TGAAACCATGGAGTGCAGGTTTACAGCTAGAGGACAGGAGCAGTGTGATTTGCTCTAA 516
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 QY 757 CACAAACTTATG 768
 Db 721 CACAAACTTATG 732

RESULT 7
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 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

DR802415 Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 730)
 Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C., Rao,K., Haller,K., Wing,K., Soderlund,C., Walbot,V. and Yu,Y.
 Maize Full-length cDNA Project
 Unpublished (2005)
 Contact: Yeisoo Yu
 Arizona Genomics Institute
 The University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9585
 Fax: 520 621 1259
 Email: yeisoo@genome.arizona.edu
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 /note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for a normalization step was conducted against the mixture of

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES
 source

RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>).

ORIGIN

Query Match 42.9%; Score 730; DB 8; Length 730;
 Best Local Similarity 100.0%; Pred. No. 8.8e-195; Mismatches 0; Indels 0; Gaps 0;
 Matches 730; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB |||||
 QY 730 TTGCAATATAAACAAGTATACAGAGGAAAGGACAGACTTATTTCTTCAAGCATTTT 671
 DB |||||

QY 946 ATCAGCTTTGAGCTATCCCAACAGAGAAATCTTAAAGTGCCTAGAAATACATGCTGTAG 1005
 DB |||||

QY 670 ATCAGCTTTGAGCTATCCCAACAGAGAAATCTTAAAGTGCCTAGAAATACATGCTGTAG 611
 DB |||||

QY 1006 TTGTGGGAAGTATGTTAATGCTCAGACCAAAATTTGAGACTCAGTTACGTGCTTTGTGG 1065
 DB |||||

QY 610 TTGTGGGAAGTATGTTAATGCTCAGACCAAAATTTGAGACTCAGTTACGTGCTTTGTGG 551
 DB |||||

QY 1066 TGAAGAACAACAGATTATGACCGTGTCTTATTTGTGAACAAGACATTTGGCAGTGGCCCTT 1125
 DB |||||

QY 550 TGAAGAACAAGATTATGACCGTGTCTTATTTGTGAACAAGACATTTGGCAGTGGCCCTT 491
 DB |||||

QY 1126 ACTTGCGAGCAATGATGCTTGTGTTGAGAAATCTCAGCGCGCTGGAGAAATCTTTGGA 1185
 DB |||||

QY 490 ACTTGCGAGCAATGATGCTTGTGTTGAGAAATCTCAGCGCGCTGGAGAAATCTTTGGA 431
 DB |||||

QY 1186 GATTAACATTAAGCAATGCAATTCAGTTCCAGTATTTGGCAGCGCTGCTGGAGGA 1245
 DB |||||

QY 430 GATTAACATTAAGCAATGCAATTCAGTTCCAGTATTTGGCAGCGCTGCTGGAGGA 371
 DB |||||

QY 1246 CCACGAGATCTCTCGACGCGCTCGACTGGCTCTCTGATCTCTGCTGGAGAGGGCG 1305
 DB |||||

QY 370 CCACGAGATCTCTCGACGCGCTCGACTGGCTCTCTGATCTCTGCTGGAGAGGGCG 311
 DB |||||

QY 1306 TGGCGCTCTTGCAGAAACATGCTCAGACTCGCAAGCCACCGCAGCAGAGGGTCTCCA 1365
 DB |||||

QY 310 TGGCGCTCTTGCAGAAACATGCTCAGACTCGCAAGCCACCGCAGCAGAGGGTCTCCA 251
 DB |||||

QY 1366 TGGGGGAAAGGCTATGCGAGGTGAAGAAATGTTCTATGAGCAACCATGGCTGAGA 1425
 DB |||||

QY 250 TGGGGGAAAGGCTATGCGAGGTGAAGAAATGTTCTATGAGCAACCATGGCTGAGA 191
 DB |||||

QY 1426 GGATCGCGCGTGTGTAAGGATGCTCTCAGAGAAATCAAGAGCACTCCAGCTTTGAG 1485
 DB |||||

QY 190 GGATCGCGCGTGTGTAAGGATGCTCTCAGAGAAATCAAGAGCACTCCAGCTTTGAG 131
 DB |||||

QY 1486 CTTTGGCGTCCCATCAGCTTCGCTTAACATGTTGAATAGATTTTACGGGCTACGCCTA 1545
 DB |||||

QY 130 CTTTGGCGTCCCATCAGCTTCGCTTAACATGTTGAATAGATTTTACGGGCTACGCCTA 71
 DB |||||

QY 1546 CTTGTTTACGGCTGTAACATGATGCACTCTGTTGCTTACTTTTTCATTCATGCT 1605
 DB |||||

QY 70 CTTGTTTACGGCTGTAACATGATGCACTCTGTTGCTTACTTTTTCATTCATGCT 11
 DB |||||

QY 1606 TTTTACCTATT 1615
 DB |||||

QY 10 TTTTACCTATT 1

RESULT 8

DR790489

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Ze mays

Ze mays

Ze mays

Ze mays

Ze mays

Ze mays

Ze mays

Ze mays

Ze mays

Ze mays

Ze mays

Ze mays

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DR790489 715 bp mRNA linear EST 27-JUL-2005
 ZM.BF00009H19.r.ZM.BFB Zea mays cDNA 5', mRNA sequence.

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 ZM.BF00009H19.r.ZM.BFB Zea mays cDNA 5', mRNA sequence.

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 ZM.BF00009H19.r.ZM.BFB Zea mays cDNA 5', mRNA sequence.

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 ZM.BF00009H19.r.ZM.BFB Zea mays cDNA 5', mRNA sequence.

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DR790489 715 bp mRNA linear EST 27-JUL-2005
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DR790489 715 bp mRNA linear EST

KEYWORDS

SOURCE

ORGANISM

Saccharum officinarum
 Saccharum officinarum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
 complex.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 879)
 Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
 The libraries that made SUCEST
 Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
 Contact: Arruda P
 Centro de Biologia Molecular e Engenharia Genética
 Universidade Estadual de Campinas
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil
 Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089
 Email: parruda@unicamp.br
 Cloning distribution: clone distribution information can be found
 through the Brazilian Clone Collection Center (BCCC) at
 http://www.bcccenter.fcav.unesp.br
 Plate: 093 row: D column: 01
 Seq primer: T7 Promoter Primer.

FEATURES

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/lab_host="DH10B"

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/note="Organ: Fourth apical stalk internodes of adult
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 (Invitrogen). The double-strand cDNAs were fractionated
 in a sepharose CL-2B 40cm-columns and fragments sizing
 between 0.8 and 1.5 Kb were directionally cloned into the
 vector. Details of each source of RNA and library
 construction can be obtained at
 http://succest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 38.7%; Score 659.4; DB 6; Length 879;
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CB661667

LOCUS

DEFINITION

CB661667

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

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CB661667

CB661667.1 GI:29665392

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 831)

Jantasuriyarat,C., Cowda,M., Haller,K., Hatfield,J., Lu,G.,
 Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
 Soderlund,C. and Wang,G.L.

Large-scale identification of expressed sequence tags involved in
 rice and rice blast fungus interaction

Plant Physiol. 138 (1), 105-115 (2005)

15888683

Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: rwing@genome.arizona.edu

PCR Primers

FORWARD: gta aac cga cgg cca gtc

BACKWARD: gga aac agc tat gac cat g

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REFERENCE 1 (bases 1 to 813)
AUTHORS   Jantacuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
          Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
          Soderlund,C. and Wang,G.L.
          Large-scale identification of expressed sequence tags involved in
          rice and rice blast fungus interaction
          Plant Physiol. 138 (1), 105-115 (2005)
15888683
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
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REFERENCE 1 (bases 1 to 753)
AUTHORS   Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H.,
          De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and
          Arruda,P.
          Endosperm-preferred expression of maize genes as revealed by
          transcriptome-wide analysis of expressed sequence tags
          Plant Mol. Biol. (2005) in press
          Contact: Arruda P

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Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br.

FEATURES source

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(DAP), seeds were cut from the ear and the upper third of
the endosperms, containing only endosperm, aleurone and
pericarpal tissues, was removed, frozen in liquid nitrogen
and stored at -800 C. Frozen endosperms were pulverized in
liquid nitrogen and total RNA was isolated according the
method of Manning (9). Poly(A)+RNA was isolated using
Oligotex-dT. cDNA libraries were constructed using
SuperScript Plasmid System for cDNA Synthesis and Plasmid
Cloning Kit as described in Vettore, et al. (2001). The
libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs
ranging from 500 to 800 bp in size were assigned as short
libraries (S10, S15, S20), and cDNAs >800 were assigned as
long libraries (L10, L15, M15, L20, L25). Unamplified
libraries were plated and individual colonies picked and
transferred to 96 well plates containing liquid circle
Grow (CG) medium supplemented with 100 mg/L of ampicillin
and 8% glycerol. Three copies of each cDNA clone were
stored at -800 C. Additional information can be found in :
Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S,
Fleisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,
A.L., da Silva, P.R. and Arruda, P. (2005)
Endosperm-preferred expression of maize genes as revealed
by transcriptome-wide analysis of expressed sequence tags.
Plant Molecular Biology (/in press/)"

Query Match 37.4%; Score 635.8; DB 7; Length 753;
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QY 1253 GATCGTCTGACGGCTCGACTGCGCTTCTGTCATCTGCTGGGAAGAGGGCGTGGCGCC 1312

ORIGIN

Db 329 GATCGTCTGACGGCTCGACTGGGCTTCTGATCTCTGCTGGGAAGAGGGCGTGGCGCC 388
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QY 1373 AAAGGGCTATGCGCAGGGTGAAGGAATGTTTCATGAGCACCACATGGCTGAGAGGATCGC 1432
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Db 509 GCGCGTGTGAAGGATGTCCTCAGGAAATCAGAGGACACTCCAGGTCTTTGAGCTTTGCC 568
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DR805335 629 bp mRNA linear EST 28-JUL-2005
ZM_BFB0030M17.f ZM_BFB Zea mays cDNA 3', mRNA sequence.
DR805335
VERSION DR805335.1 GI:71421191
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 629)
Rao, K., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C.,
Kim, H., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.
Maize Full-length cDNA Project
Unpublished (2005)
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The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
Plate: 0030 row: M column: 17.
Location/Qualifiers
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tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="DH10B T1 phage resistant"
/clone_lib="ZM_BFB"

FEATURES
source

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/clone_lib="ZM_BFB"

/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:
NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a Gateway compatible vector.
permitting clone movement to new vector backbones for
expression in diverse host cells using recombination
rather than restriction enzymes. poly(A)+ mRNA was
prepared by Invitrogen, and equimolar amounts of RNA from

each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>).

ORIGIN

Query Match	36.5%	Score 621;	DB 8;	Length 629;
Best Local Similarity	99.2%	Pred. No. 6.2e-164;		
Matches 624;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;

QY	998	TGCTGTAGTTTGGGAAGTATGTTAATGCTCAGACCAAAATTGAGACTCAGTTAGTGA	1057
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QY	1058	CTTTGTGTGAAGAACACGATTCATGACCGTGTCCATTTTGTGAACAGACATTTGGCAGT	1117
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QY	1298	GGAGGGCGTGGCGCCTTTTGCAAGAAACATCGTCAGACTCGCAAGCCACGCCGAGCAGAG	1357
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QY	1358	GGTCTCCATGGGGGAAAGGGCTATGGCAGGGTGAAGGAAATGTTTCATGGAGCACACAT	1417
DB	269	GGTCTCCATGGGGGAAAGGGTATGGCAGGGTGAAGGAAATGTTTCATGGAGCCCCACAT	210
QY	1418	GGCTGAGAGGATCGCGGGCGTGTGAAGGATGTCTGAGGAAATCACAGGAGCAGTCCAG	1477
DB	209	GGCTGAGAGGATCGCGGGCGTGTGAAGGATGTCTGAGGAAATCACAGGAGCAGTCCAG	150
QY	1478	GTCTTTGAGCTTTGCCGTGCCCATCAGCTTTGCCGTAACTGTTGAACATAGATTTTACGGGC	1537
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QY	1538	TAGGCTACGTGGTTCAGGCTGTAACTGATAGATTCGACTCTGTTGGTCTACTTTTTCAC	1597
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Job time : 7109 secs

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